

GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: February 21, 2006, 21:39:11 ; Search time 231 Seconds
(without alignments)
494,786 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPIKVGDAlPAVEVFGER VEPDGITGLTCSLAPNITSQL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 Bseqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : UniProt 05 80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	830	100.0	214	PRDX5_HUMAN
2	830	100.0	214	061AF2_HUMAN
3	822	99.0	215	PRDX5_CERAB
4	818	98.6	215	PRDX5_PAPHA
5	767	92.4	210	PRDX5_MOUSE
6	767	92.4	213	PRDX5_RAT
7	763	91.9	213	06G2Z7_RAT
8	761	91.7	162	09GLW8_PIG
9	747	90.0	219	PRDX5_BOVIN
10	727	87.6	211	09D6XZ_MOUSE
11	583.5	70.3	189	06GPY3_XENLA
12	536.5	64.6	162	05028_BRARE
13	524	63.1	188	08T5Q7_BRABE
14	494.5	59.6	157	05UG08_AEDAR
15	486.5	58.6	246	07PUM1_ANODA
16	484	58.3	168	0694AB_GLOMR
17	483	58.2	157	06XHE3_DROTA
18	481	58.0	190	09604_DROME
19	475.5	57.3	175	07PUPA_ANOGA
20	408	49.2	89	091Y9_MOUSE
21	400.5	48.3	185	08MUNO_PYRUR
22	355.5	42.8	184	05A2B7_CANAL
23	355.5	42.8	184	05A2G3_CANAL
24	354.5	42.2	220	04WLS4_ASPTU
25	341.5	41.1	167	07WMO6_BORER
26	341.5	41.1	183	07WBB8_BORER
27	337.5	40.7	167	07VVF4_BORER
28	336.5	40.5	188	05B623_EMBEN
29	321	38.7	168	06CUCU_METCA
30	318.5	38.4	185	06BZD0_DEBRA
31	317	38.2	172	08G255_BRUSU

RESULT	1
ID	PRDX5_HUMAN
STANDARD	PRT; 214 AA.
PRT	PRDX5_HUMAN; Q9UBU5; Q9UJU4; Q9UKX4;
AC	P30044; Q9UBU5; Q9UJU4; Q9UKX4;
DT	01-APR-1993 (Rel. 25, Created)
DT	28-FEB-2005 (Rel. 41, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Peroxiredoxin 5 mitochondrial precursor (EC 1.11.1.15) (Prx-V)
DE	(Peroxisomal antioxidant enzyme) (PLP) (thioredoxin reductase)
DE	(Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOEB166)
DE	(TPx type VI) (Liver tissue cDNA clone 71B) (Alu corepressor 1).
GN	Name=PRDX5; Synonyms=ACR1; ORFNames=SSB110;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Osteichthyes; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TAXID=9606;
RN	[1] NUCLEOTIDE SEQUENCE.
RP	RP
RA	Kim I.H., Jeong W.,
RT	"A new type of human triol peroxidase (Human TPx type VI)." ; Submitted (SSP-1999) to the EMBL/GenBank/DDBJ databases.
RN	[2] NUCLEOTIDE SEQUENCE.
RP	RP
RA	MEDLINE=2014535; PubMed=10679306; DOI=10.1006/bbrc.2000.2231;
RA	Zhou Y., Kok K.H., Chun A.C.S., Wong C.M., Wu H.W., Lin M.C.M.,
RA	Fung P.C.W., Kung H.-F., Jin D.-Y.,
RT	"Mouse peroxiredoxin V is a thioredoxin peroxidase that inhibits p53-induced apoptosis";
RT	Biochem. Biophys. Res. Commun. 268:921-927(2000).
RL	RL
RN	[3] NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RP	MEDLINE=9944545; PubMed=10514471; DOI=10.1074/jbc.274.42.29897;
RA	Yamashita H., Avraham R.A., Jiang S., London R., Van Veldhoven P.P., Subramani S., Rogers R.A., Avraham H.-H.
RA	"Characterization of human and murine PMP20 peroxisomal proteins that exhibit antioxidant activity in vitro.";
RL	J. Biol. Chem. 274:29897-29904(1999).
RN	[4] NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RP	MEDLINE=9945292; PubMed=10521424; DOI=10.1074/jbc.274.3.30451;
RA	Knops B., Cliffe A., Bogard C., Arsalane K., Wattiez R., Hermans C., Duconseille E., Faugeron P., Bernard A.,
RT	"Cloning and characterization of AOB166, a novel mammalian antioxidant enzyme of the peroxiredoxin family.";
RT	antioxidant enzyme of the peroxiredoxin family. J. Biol. Chem. 274:30451-30458(1999).
RL	RL
RN	[5] NUCLEOTIDE SEQUENCE, MUTAGENESIS, AND CHARACTERIZATION.
RP	MEDLINE=20347113; PubMed=10751410; DOI=10.1074/jbc.M001942200;
RA	Seo M.S., Kang S.W., Kim K., Baines T.C., Lee T.H., Rhee S.G.,
RT	"Identification of a new type of mammalian peroxiredoxin that forms an intramolecular disulfide as a reaction intermediate.";
RT	J. Biol. Chem. 275:20346-20354 (2000).
RL	Q89255 brucella su

Q8Yfr4 brucella me
Q57EP3 brucella ab
Q9A312 caulobacter
Q985V8 rhabdium 1
Q51NG6 magaporthe
Q75AS4 ashyba goss
Q753H3 neuocr
Q87GM2 vibrio para
Q51m28 silicibacte
Q412K2 burkhholderi
Q8E8H3 shewanella
Q63GK3 burkhholderi
Q4tna8 erythrobact
Q8Wha4 agrobacteri

DR	SWISS-2DPAGE; P30044; HUMAN.
DR	OGR2; P30044; -.
DR	ExaembL; ENSG0000126432; Homo sapiens.
DR	MEDLINE=99195471; PubMed=10095767;
DR	Kropotov A., Sedova V., Ivanov V., Sazeeva N., Tomilin A., Tomilin N., Krutkina R., Oei S.L., Grieshaber J., Buchlow G., Tomilin N.; A novel human R-, DNA-binding protein with sequence similarity to a subfamily of redox protein which is able to repress RNA-polymerase-III-driven transcription of the Alu-family retroposons in vitro.;
DR	Eur. J. Biochem. 260:336-346 (1999).
[7]	
RC	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC	TISSUE=Adrenal Gland.
RC	MEDLINE=20402571; PubMed=10931946; DOI=10.1073/pnas.160270997;
RC	Guo R.-M., Huang Z.-G., Peng H.-D., Huang Q.-H., Ren S.-X., Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H., Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J., Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M., Huang G.-Y., Yu Z., Chen M.-D., Chen J.-L.; Gene expression profiling in the human hypothalamus-pituitary-adrenal axis and full-length cDNA cloning.;
RC	Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548 (2000).
[8]	
RC	NUCLEOTIDE SEQUENCE [mRNA].
RC	Zhang W., Li N., Wan T., Cao X.; Submitted (MARR-2000) to the EMBL/GenBank/DDBJ databases.
RN	PROTEIN SEQUENCE OF 54-63.
RC	TISSUE=Liver;
RC	MEDLINE=93162045; PubMed=12866669;
RA	Hochstrasser D.-P., Frutiger S., Paquet N., Bairoch A., Ravier F., Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R., Appel R.D., Hughes G.J.; Human liver protein map: a reference database established by microsequencing and gel comparison.;
RL	Electrophoresis 13:992-1001(1992).
[10]	
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS); MEDLINE=21410064; PubMed=11518528; DOI=10.1006/jmbi.2001.4853;
RA	Declercq J.-P., Evrard C., Cliffe A., Stricht D.V., Bernard A., Knops B.;
RT	"Crystal structure of human peroxiredoxin 5, a novel type of mammalian peroxiredoxin at 1.5-Å resolution.";
RL	J. Mol. Biol. 311:751-759(2001).
CC	-I- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with reducing equivalents provided through the thioredoxin system. involved in intracellular redox signaling.
CC	-I- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H ₂ O + ROH.
CC	-I- SUBUNIT: Monomer.
CC	-I- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic.
CC	-I- ALTERNATIVE PRODUCTS:
CC	Event Alternative initiation; Comment=2 Isoforms, Mitochondrial (shown here) and Cytoplasmic-peroxisomal are produced by alternative initiation;
CC	-I- TISSUE SPECIFICITY: Widely expressed.
CC	-I- SIMILARITY: Belongs to the peroxiredoxin 2 family.
CC	-----
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC	-----
DR	EMBL; AJ249483; CBR62210.1; -; mRNA.
DR	EMBL; AP197952; RAF04856.1; -; mRNA.
DR	EMBL; AP124993; RAF27531.1; -; mRNA.
DR	EMBL; AP10731; RAF03750.1; -; mRNA.
DR	EMBL; AP231705; RAF7889.1; -; mRNA.
DR	EMBL; AP112212; RAF17200.1; -; mRNA.
DR	EMBL; AP242525; RAF99605.1; -; mRNA.
DR	EMBL; AP1440; X-ray; A/B/C/D/E/F/G/H=54-214.
DR	PDB; 1HD2; X-ray; A=54-214.
DR	PDB; 1003; X-ray; A/B/C/D/E/F/G/H=54-214.
DR	PDB; 1JRM; X-ray; A=54-214.
DR	-----
DR	OG2; P30044; -.
DR	ExaembL; ENSG0000126432; Homo sapiens.
DR	HGNC; HGNC:9355; PRDX5.
DR	H-InvDB; HInv021287; -.
DR	MIM; 606583; -.
DR	GO; GO-0005739; C:mitochondrion; TAS.
DR	GO; GO-0005777; C:peroxisome; TAS.
DR	GO; GO-0005949; P:inflammatory response; TAS.
DR	GO; GO-0005954; P:respiratory gaseous exchange; TAS.
DR	GO; GO-0005985; P:response to oxidative stress; TAS.
DR	InterPro; IPR000666; ApbC-TSA.
DR	InterPro; IPR012336; Thioredoxin-like.
DR	InterPro; IPR012335; Thioredoxin_fold.
DR	Pfam; PF00578; ApbC-TSA; 1.
KW	3D-structure; Alternative initiation; Direct protein interaction; Mitochondrion; Oxidoreductase; Peroxidase; Peroxisome; Polymorphism; Redox-active center; Transit peptide.
KW	Transit 1; Motif 1; Motif 2; Motif 3; Motif 4; Motif 5; Motif 6; Motif 7; Motif 8; Motif 9; Motif 10; Motif 11; Motif 12; Motif 13; Motif 14; Motif 15; Motif 16; Motif 17; Motif 18; Motif 19; Motif 20; Motif 21; Motif 22; Motif 23; Motif 24; Motif 25; Motif 26; Motif 27; Motif 28; Motif 29; Motif 30; Motif 31; Motif 32; Motif 33; Motif 34; Motif 35; Motif 36; Motif 37; Motif 38; Motif 39; Motif 40; Motif 41; Motif 42; Motif 43; Motif 44; Motif 45; Motif 46; Motif 47; Motif 48; Motif 49; Motif 50; Motif 51; Motif 52; Motif 53; Motif 54; Motif 55; Motif 56; Motif 57; Motif 58; Motif 59; Motif 60; Motif 61; Motif 62; Motif 63; Motif 64; Motif 65; Motif 66; Motif 67; Motif 68; Motif 69; Motif 70; Motif 71; Motif 72; Motif 73; Motif 74; Motif 75; Motif 76; Motif 77; Motif 78; Motif 79; Motif 80; Motif 81; Motif 82; Motif 83; Motif 84; Motif 85; Motif 86; Motif 87; Motif 88; Motif 89; Motif 90; Motif 91; Motif 92; Motif 93; Motif 94; Motif 95; Motif 96; Motif 97; Motif 98; Motif 99; Motif 100; 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Motif 599968; Motif 599969; Motif 599960; Motif 599961; Motif 599962; Motif 599963; Motif 599964; Motif 599965; Motif 599966; Motif 599967; Motif 599968; Motif 599969; Motif 599970; Motif 599971; Motif 599972; Motif 599973; Motif 599974; Motif 599975; Motif 599976; Motif 599977; Motif 599978; Motif 599979; Motif 599970; Motif 599971; Motif 599972; Motif 599973; Motif 599974; Motif 599975; Motif 599976; Motif 599977; Motif 599978; Motif 599979; Motif 599980; Motif 599981; Motif 599982; Motif 599983; Motif 599984; Motif 599985; Motif 599986; Motif 599987; Motif 599988; Motif 599989; Motif 599980; Motif 599981; Motif 599982; Motif 599983; Motif 599984; Motif 599985; Motif 599986; Motif 599987; Motif 599988; Motif 599989; Motif 599990; Motif 599991; Motif 599992; Motif 599993; Motif 599994; Motif 599995; Motif 599996; Motif 599997; Motif 599998; Motif 599999; Motif 599990; Motif 599991; Motif 599992; Motif 599993; Motif 599994; Motif 599995; Motif 599996; Motif 599997; Motif 599998; Motif 599999; Motif 5999910; Motif 5999911; Motif 5999912; Motif 5999913; Motif 5999914; Motif 5999915; Motif 5999916; Motif 5999917; Motif 5999918; Motif 5999919; Motif 5999910; Motif 5999911; Motif 5999912; Motif 5999913; Motif 5999914; Motif 5999915; Motif 5999916; Motif 5999917; Motif 5999918; Motif 5999919; Motif 5999920; Motif 5999921; Motif 5999922; Motif 5999923; Motif 5999924; Motif 5999925; Motif 5999926; Motif 5999927; Motif 5999928; Motif 5999929; Motif 5999920; Motif 5999921; Motif

RESULT 2
Q1AF2_HUMAN
ID Q1AF2_HUMAN PRELIMINARY; PRT; 214 AA.
AC Q1AF2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE PRDX5 protein.
GN Name=PRDX5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo;
OX NCBI_TaxID=9606;
RN [1];
RP NITROLEUTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
CC EMBL: CR457203; CAG33494.1; -; mRNA.
DR PRDX5 protein.
DR SMR; Q1AF2; 54-214.
DR Ensembl; ENSC0000126432; Homo sapiens.
DR InterPro; IPR00866; APcC-TSA.
DR InterPro; IPR012336; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF00578; APcC-TSA; 1.
DR KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.
SQ SEQUENCE 214 AA; 22026 MW; 2FF21210809823E CRC64;
Best Local Similarity 100.0%; Score 830; DB 2; Length 214;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 1 MAPIKGDAIPAVEVFEGERGPKNKUNLAEFLFGKKGKVLFQVGAFTPGCSKTHLPGFVEQA 60
Db 53 MAPIKGDAIPAVEVFEGERGPKNKUNLAEFLFGKKGKVLFQVGAFTPGCSKTHLPGFVEQA 112
Qy 61 BALKAKGIVQVACISVNDAFVTGEGRAHKAEGKVKRLLADPTGAFGKETDLDLDSVSI 120
Db 113 BALKAKGIVQVACISVNDAFVTGEGRAHKAEGKVKRLLADPTGAFGKETDLDLDSVSI 172
Qy 121 FGNRRLKRPSMWWODGIVKVALNVEPDGTGKTCISLAPNTISQL 162
Db 173 FGNRRLKRPSMWWODGIVKVALNVEPDGTGKTCISLAPNTISQL 214

RESULT 3
PRDX5_CERAE
ID PRDX5_CERAE STANDARD; PRT; 215 AA.
AC Q9GLW7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Peroxiredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)
DE (Thioredoxin reductase).
Name=PRDX5;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Cercopithecus.
OC NCBI_TaxID=9534; [1]

RESULT 4
PRDX5_PAPHA
ID PRDX5_PAPHA STANDARD; PRT; 215 AA.
AC Q9GLW9;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAR-2005 (Rel. 47, Last annotation update)
DE Peroxiredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)
DE (Thioredoxin reductase).
Name=PRDX5;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Cercopithecus.
OC NCBI_TaxID=9534; [1]

RESULT 5
MAPIKGDAIPAVEVFEGERGPKNKUNLAEFLFGKKGKVLFQVGAFTPGCSKTHLPGFVEQA 112
RA Knoops B., Charif R.;
RT Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RL -!
CC -!- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with
CC reducing equivalents provided through the thioredoxin system.
CC Involved in intracellular redox signaling (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic
CC (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, Mitochondrial (shown here) and
CC Cytoplasmic-peroxisomal, are produced by alternative initiation;
CC -!- SIMILARITY: Belongs to the peroxiredoxin 2 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC DR EMBL; AF110736; AMG13453.2; -; mRNA.
CC DR HSSE; P30044; 1HD2.
CC DR SMR; Q9GLW7; 55-215.
CC DR InterPro; IPR00866; APcC-TSA.
CC DR InterPro; IPR012336; Thioredoxin-like.
CC DR InterPro; IPR012335; Thioredoxin_fold.
CC DR Pfam; PF00578; APcC-TSA; 1.
CC DR Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;
CC KW Peroxidase; Peroxisome; Redox-active center; Transit peptide.
CC FT TRANSIT 1 Mitochondrion (Potential).
CC INIT-MET 54 54 For isoform Cytoplasmic-peroxisomal.
CC FT CHAIN 55 215 Peroxiredoxin 5, isoform.
CC FT CYP 55 215 Cytoplasmic-peroxisomal.
CC FT CHAIN MOTIF 213 215 Peroxiredoxin 5, isoform Mitochondrial.
CC FT DISULFID 101 205 Microbody targeting signal (By similarity).
CC FT DISULFID 101 205 Redox-active (By similarity).
SQ SEQUENCE 215 AA; 22237 MW; 7C9B45C1B9517B78 CRC64;
Best Local Similarity 99.0%; Score 822; DB 1; Length 215;
Matches 160; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Query Match 1 MAPIKGDAIPAVEVFEGERGPKNKUNLAEFLFGKKGKVLFQVGAFTPGCSKTHLPGFVEQA 60
Qy 1 MAPIKGDAIPAVEVFEGERGPKNKUNLAEFLFGKKGKVLFQVGAFTPGCSKTHLPGFVEQA 60
Db 54 MAPIKGDAIPAVEVFEGERGPKNKUNLAEFLFGKKGKVLFQVGAFTPGCSKTHLPGFVEQA 113
Qy 61 BALKAKGIVQVACISVNDAFVTGEGRAHKAEGKVKRLLADPTGAFGKETDLDLDSVSI 120
Db 114 BALKAKGIVQVACISVNDAFVTGEGRAHKAEGKVKRLLADPTGAFGKETDLDLDSVSI 172
Qy 121 FGNRRLKRPSMWWODGIVKVALNVEPDGTGKTCISLAPNTISQL 162
Db 174 FGNRRLKRPSMWWODGIVKVALNVEPDGTGKTCISLAPNTISQL 215

OX NCBI_TaxID=9557;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Knoops B., Cherif H.;
 RT "Cloning and characterization of baboon A0EB166/PRDX5.";
 RL to the EMBL/GenBank/DDBj databases.
 CC -!- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with
 reducing equivalents provided through the thioredoxin system.
 CC involved in intracellular redox signaling (BY similarity).
 CC -!- CATALYTIC ACTIVITY: 2 R-SH + ROOH = R'-S-S-R + H₂O + ROH.
 CC -!- SUBUNIT: Monomer (BY similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic
 (BY similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 Event:Alternative initiation;
 Comment=2 isoforms, Mitochondrial (shown here) and
 Cytoplasmic+peroxisomal, are produced by alternative initiation;
 CC -!- SIMILARITY: Belongs to the peroxiredoxin 2 family.
 This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC EMBL: AFI10734; AAG13451.2; - ; mRNA.
 DR HSSP: P30044; IMD2.
 DR SMR_O9GIW9; 55-215.
 DR InterPro: IPR00866; AhpC-TSA.
 DR InterPro: IPR012336; Thioredoxin_fold.
 DR InterPro: IPR012335; Thioredoxin_fold.
 DR Pfam: PF00578; AhpC-TSA; 1.
 DR Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;
 KW Peroxidase; Peroxisome; Redox-active center; Transit peptide.
 FT TRANSIT 1 ? Mitochondrion (Potential).
 FT INITI MET 54 54 For isoform Cytoplasmic+peroxisomal.
 FT CHAIN 55 215 Paroxiredoxin 5, isoform
 FT MOTIF 213 215 Cytoplasmic+peroxisomal.
 FT DISULFID 101 205 Microbody targeting signal (BY
 SQ SEQUENCE 215 AA; 22166 MW; 65183A24535C1617 CRC64;
 Query Match 98.6%; Score 818; DB 1; Length 215;
 Best Local Similarity 98.1%; Pred. No. 1 le-64;
 Matches 159; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MAPIKVGDPAIRAVEVFGEPGNKVNLALFKKGKGVLFVGKRAFTPGCSKTHLPGYEOA 60
 Db 54 MAPIKVGDPAIRAVEVFGEPGNKVNLALFKKGKGVLFVGKPGATPGCSKTHLPGFVEQA 113
 Qy 61 EALKAKGQYQVACLSVDAFVYGEWGRAHKAECVKVLLADPGAFGETDILDDSVI 120
 Db 114 EALKAKGQYQVACLSVDAFVYGEWGRAHKAECVKVLLADPGAFGETDILDDSVI 173
 Qy 121 FGURRLKPFPSMWQDGIVKALNVEPDGTGLTSLAPNITSQL 162
 Db 174 FGURRLKPFPSMWQDGIVKALNVEPDGTGLTSLAPNISQL 215
 RESULT 5
 PRDX5_MOUSE STANDARD; PRT; 210 AA.
 ID PRDX5_MOUSE STANDARD; PRT; 210 AA.
 AC P99025; Q9QX45; Q9QZ5;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Peroxiredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)
 DE (Peroxisomal antioxidant enzyme) (PPL) (Thioredoxin reductase)
 DE (Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOB166)
 DE (Liver tissue 2D-page spot 2D-0014IV).
 GN Name=Prdx5; Synonyms=Prdx6;
 CC [2]
 NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
 RX MEDLINE=93445545; PubMed=10514471; DOI=10.1074/jbc.274.42.29897;
 RA Yamashita H., Abraham S., Jiang S., London R., Van Veldhoven P.,
 RA Subramani S., Rogers R.A., Avrath A.H.;
 RT "Characterization of human and murine PMP20 peroxisomal proteins that
 exhibit antioxidant activity in vitro.";
 RL J. Biol. Chem. 274:29897-29904 (1999).
 RN [3]
 NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=C3H/HeJ; TISSUE=Lung;
 RN MEDLINE=93452939; PubMed=10521424; DOI=10.1074/jbc.274.43.30451;
 RA Knoops B., Cliffe A., Bogard C., Arsalane K., Wattiez R., Hermans C.,
 RA Duconceau E., Palmagne P., Bernard A.;
 RT "Cloning and characterization of AOB166, a novel mammalian
 antioxidant enzyme of the peroxiredoxin family.";
 RL J. Biol. Chem. 274:30451-30458 (1999).
 RN [4]
 NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20518665; PubMed=10753630; DOI=10.1006/bbrc.2000.2430;
 RA Lee T.H., Kim S.J., Kang S.W., Lee K.K., Rhee S.G., Yu D.Y.;
 RT "Molecular cloning and characterization of the mouse Peroxiredoxin V
 gene.";
 RL Biochem. Biophys. Res. Commun. 270:356-362(2000).
 RN [5]
 NUCLEOTIDE SEQUENCE [LARGE SCALE RNA].
 RX STRAIN=C57BL/6J; TISSUE=Kidney;
 RA MEDLINE=2235633; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osatō N., Saito Y., Suzuki H., Yamamoto I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bratt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani B.A., Fletcher C.F.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Jarvis E.D.,
 RA Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.L.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King J.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavani W.J., Pertelet G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed D.J., Reid J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyñshaw-Boris A., Yanagisawa M., Yang J., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hironzane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Wakai K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotsiki K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shihara K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analyses of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 [6]
 NUCLEOTIDE SEQUENCE [LARGE SCALE RNA].
 RC TISSUE=Mammary tumor;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-247 <HEI>
 A;Cross-references: UNIPROT:09KNU3; UNIPARC:UPI00000C3360; GB:AE04330; GB:AE003852; NID:10952301
 A;Experimental source: serogroup O1; strain N1691; biotype El Tor
 C;Genetics:
 A;Gene: VC2637
 A;Map position: 1

Query Match 29.3%; Score 243.5; DB 2; Length 247;
 Best Local Similarity 38.8%; Pred. No. 4.5e-15;
 Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 4;

QY 5 KVGDALIPAV--EVFEGEPGNKVNLAELFKKGKKGVLFGVPGAFPTPGCSKTHLPGVQEAEAL 62
 9 KEGQTRIPQVTPTRQDADWNTVNTSDBELFKKGKTKVIVFSLPQAFPTPCSSSHLPRYNELEPFLV 68

QY 63 LKAKGVQVVAQCLSVNDAFYTGCBWGAHKAKGKGVRLADPGAFGKGETDILDDSVSIRG 122
 69 FKEHGVDLILVSVNDAFTVNAKWDQNAAD-NITFIDGNGEFTDGMGLVDKNDLG-FG 126

QY 123 NRRLKRKPSMVYQDGVKALANVDPGTG 149
 127 -KRSRYSMLVKNGYVERMTEPNERG 152

RESULT 14

AB0477 probable peroxiredoxin/glutaredoxin family protein YPO3916 [imported] - *Yersinia pestis*
 C;Species: *Yersinia pestis*
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AB0477
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.;
Nature 413, 523-527, 2001
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AB0477
 A;status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-243 <KUR>
 A;Cross-references: UNIPROT:Q8ZA95; UNIPARC:UPI00000DCAA0; GB:AL590842; PIDN: CAC93382.1;
 C;Genetics:
 C;Gene: YPO3916

Query Match 27.2%; Score 225.5; DB 2; Length 243;
 Best Local Similarity 36.6%; Pred. No. 2e-13; Matches 53; Conservative 27; Mismatches 60; Indels 5; Gaps 4;

QY 7 GDAIAPV--EVFEGEPGNKVNLAELFKKGKKGVLFGVPGAFPTPGCSKTHLPGVQEAEAL 64
 7 GKKVQVQFTFTRQDQWIDVTDLFSNKTVIVFSLPQAFPTPCSSSHLPRYNELEPFLV 66

QY 65 AKGVQVACISVNDAAFTGKGRAHKAEGKVRLLADPGAFGKGETDILDDSVSIRG 124
 67 QHGVSILCVNDTVMNNAKWDQNAAD-NITFIDGNGEFTDGMGLVDKNDLG-FGPR 124

QY 125 RIKRPSMVYQDGVKALANVDPGTG 149
 125 SW-RVSMVLVNGVWKEKMFVERPNKG 148

RESULT 15

I6154保守性 hypothetical protein HI0572 - *Haemophilus influenzae* (strain Rd KW20)

C;Species: *Haemophilus influenzae*

Query Match 26.4%; Score 219.5; DB 2; Length 241;
 Best Local Similarity 36.3%; Pred. No. 7.3e-13; Matches 53; Conservative 27; Mismatches 59; Indels 7; Gaps 5;

QY 7 GDAIAPVEVFEGEPGNK--VNLAELFKKGKKGVLFGVPGAFPTPGCSKTHLPGVQEAEAL 63
 6 GKKVQVQ-TPTRQDQDKWDVTSSELFQDKTVIVFSLPQAFPTPCSSSHLPRYNELEPFLV 64

QY 64 KAKGVQVACISVNDAAFTGKGRAHKAEGKVRLLADPGAFGKGETDILDDSVSIRG 123
 65 KKGVQVDDLILVSVNDAFTVNAKWDKEDEKSB-NISFIDGNGEFTDGMGLVKGKEDLG-FG 121

QY 124 RRIKRPSMVYQDGVKALANVDPGTG 149
 122 KRSRYSMLVKNGYVERMTEPNERG 147

Search completed: February 21, 2006, 21:46:54
 Job time : 40 secs

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C;Accession: I64154
 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Karpness, B.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Li, L.I.; Glodek, A.; Kelley, J.M.; Weiman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995
 A;Authors: Grahm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A;Reference number: A64000; MUID:9530630; PMID:7542800
 A;Accession: I64154
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-241 <TIGR>
 A;Cross-references: UNIPROT:P44758; UNIPARC:UPI000139ABD; GB:U32739; GB:L42023; NID:915



SQ	SEQUENCE	162 AA:	17324 MW:	8C6F98D1FA3B74D5 CRC64;	FT	CHAIN	?	219	Peroxiredoxin 5, isoform Mitochondrial.
Query Match	91.7%	Score 761;	DB 2;	Length 162;	FT	CHAIN	?	219	Microbody targeting signal (By similarity).
Best Local Similarity	90.7%	Score 761;	DB 2;	Length 162;	FT	MOTIF	217	219	Microbody targeting signal (By similarity).
Matches	147;	Conservative	6;	Mismatches 9;	FT	DISUIFID	105	209	Redox-active (By similarity).
QY	1	MAPIKVGDAIPAVEVFEGEPGNKVNLAELFKGKGKVLFVGPGAFTPGCKTHLPQFVEQA	60	FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;	Query Match 90.0%; Score 747; DB 1; Length 219;
Db	1	MAPIKVGDAIPSVVFEGEPGNKVNLAELFKGKGKVLFVGPGAFTPGCKTHLPQFVEQA	60	FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;	Best Local Similarity 87.0%; Pred. No. 2.4e-58; Mismatches 9;
QY	61	EALKAKGKVQVACVSLVNDVFTVEMWGRAHKABSKVRLADPTGAFGKETDILLDDSLVSI	120	FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;	Matches 141; Conservative 12; Mismatches 9;
Db	61	EALKAKGKVQVACVSLVNDVFTVEMWGRAHKABSKVRLADPTGAFGKETDILLDDSLVSI	120	FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;	Indels 0; Gaps 0;
QY	121	FGNRLKRFKFSMVIEDGIVKSLVNPDDGTGLTCSLAPNIIQL	162	FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;	QY 61 EALKAKGKVQVACVSLVNDVFTVEMWGRAHKABSKVRLADPTGAFGKETDILLDDSLVSI 120
Db	121	FGNRLKRFKFSMVIEDGIVKSLVNPDDGTGLTCSLAPNIIQL	162	FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;	Db 58 MAPIKVGDAIPSVVFEGEPGNKVNLAELFKGKGKVLFVGPGAFTPGCKTHLPQFVEQA 60
QY	121	FGNRLKRFKFSMVIEDGIVKSLVNPDDGTGLTCSLAPNIIQL	162	FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;	QY 61 EALKAKGKVQVACVSLVNDVFTVEMWGRAHKABSKVRLADPTGAFGKETDILLDDSLVSI 120
Db	121	FGNRLKRFKFSMVIEDGIVKSLVNPDDGTGLTCSLAPNIIQL	162	FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;	Db 58 MAPIKVGDAIPSVVFEGEPGNKVNLAELFKGKGKVLFVGPGAFTPGCKTHLPQFVEQA 60
RESULT 9					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
PRDX5_BOVIN					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
ID PRDX5_BOVIN					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
AC Q8BGII_					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DT 28-FEB-2003 (Rel. 41, Created)					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DT 10-MAY-2005 (Rel. 47, Last annotation update)					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DE Peroxiredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DB (Thioredoxin reductase).					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
GN Name=PRDX5;					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
OS Bovinus (Bovine)					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
OC Bovidae; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
OX NCBI_TAXID=9913;					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RN [1]					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RP NUCLEOTIDE SEQUENCE.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RC TISSUE=Liver;					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RA Leyens G., Donnay I., Knoops B.,					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RT "Cloning of 4 new bovine peroxiredoxins, and screening of the complete peroxiredoxin family in different bovine tissues."					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RL Submitted (SBB-2000) to the EMBL/GenBank/DBJ databases.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC -!- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with reducing equivalents provided through the thioredoxin system.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC -!- INVOLVED: Involved in intracellular redox signaling (By similarity).					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROH = R'-S-S-R' + H2O + ROH.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC -!- SUBUNIT: Monomer (By similarity)					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC -!- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic (By similarity).					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC -!- ALTERNATIVE PRODUCTS:					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC Event=Alternative initiation;					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC Comment=2 isoforms, Mitochondrial (shown here) and					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC Cytoplasmic+peroxisomal, are produced by alternative initiation;					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC -!- SIMILARITY: Belongs to the Peroxiredoxin 2 family.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC EMBL: AP30564; AAEG3661.1; -; mRNA.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC HSPB; P31045; 1H22.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
CC DR Q8BGII_;					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DR InterPro: IPR002866; Thioredoxin-like.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DR IntePro: IPR012336; Thioredoxin-like.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DR InterPro: IPR012335; Thioredoxin_fold.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DR PR00578; AP0C-TSA; 1.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
DR KW Alternative; Antioxidant; Mitochondrion; Oxidoreductase; Peroxidase; Peroxisome; Redox-active center; Transient peptide.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
FT TRANSIT 1 ?					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
FT INIT_MET 58 58					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
FT CHAIN 59 219					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RC NUCLEOTIDE SEQUENCE.					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RC STRAIN=C57BL/6J; TISSUE=tongue;					FT	SEQUENCE	219 AA:	23211 MW:	93C9BD794A71581 CRC64;
RESULT 10					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
PRDX5_MOUSE					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
ID Q9D6X2_MOUSE PRELIMINARY;					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
AC Q9D6X2_					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
DT 01-JUN-2001 (TREMBL; 17, Created)					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
DT 01-JUN-2001 (TREMBL; 23, Last annotation update)					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310046N07 product:peroxiredoxin 6, full insert					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
DE sequence.					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
GN Name=Prdx5;					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
OS Mus musculus (Mouse)					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
OC Mammalia; Eutheria; Bovidae; Muridae; Murinae; Mus.					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
RC NUCLEOTIDE SEQUENCE.					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
STRAIN=C57BL/6J; TISSUE=tongue;					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
MDLINE=9227953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
RA Carnici P., Hayashizaki Y., "High-efficiency full-length cDNA cloning.", Meth. Enzymol. 303:19-44(1999).					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
RA Kawai J., Shinagawa A., Shiba K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi H., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamaka I., Saito T., Okazaki T., Gotoh O., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Pleischmann W., Gaasterland T., Glassi C., King P., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pessole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Borrelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Sato T., Shiba Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynnshaw-Borisi A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S., Hayasizaki Y., "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
RA [3]					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;
RC NUCLEOTIDE SEQUENCE.					FT	SEQUENCE	211 AA:	23211 MW:	93C9BD794A71581 CRC64;

Qy	64 KAKGVQVVAQLSINDAFTGEGWRAHKAEGKVLLADPTGTCGKETDILID-DSVSIPIG 122
Db	62 LRAKGDEVACISVNDVFMASANGKQNGADGKVRMADPTGAFKAVDILVNNQDIPV 121
Qy	90 KSRGAIVVACISVNDVFMASANGKQNGADGKVRMADPTGAFKAVDILVNNQDIPV 149
Db	123 NRRLRKFSNVQDGIVKALNVEPDGGLTCSLAPNISQL 162
Qy	150 NQRKRFSNVQDGIVKAINVNEBDGKAINVNEBDGKTCAGLNLISQL 189
RESULT 12	
Q502C8_BRAE	
ID Q502C8_BRAE PRELIMINARY; PRT; 162 AA.	
AC	
DT 13-SEP-2005 (TREMBlrel. 31, Created)	
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)	
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)	
DE Hypothetical protein zgc:112318.	
GN HypNames=zgc:112318;	
OS Brachydanio rerio (zebrafish) (Danio rerio).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC Cyprinidae; Danio.	
OX NEBI_TaxID=7955;	
RP NUCLEOTIDE SEQUENCE.	
RX TISSUE=Eye;	
RX MEDLINE=22388257; PubMed=12479792; DOI=10.1073/pnas.242603899;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA Klausner R.D., Collins F.S., Wagner L., Shammam C.M., Schuler G.D.,	
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaeffer N.K.,	
RA Diatchenko L., Marsusina K., Farmer A.A., Cubranit T.L., Scheetz T.E.,	
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Hong L.,	
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., prange C.,	
RA Raha S.S., Loqueland J.A., Peters G.J., Abramson R.D., Mullany S.J.,	
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.W.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,	
RA Villalon D.M., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA Fahey J., Heitton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA Butterfield Y.S.N., Kozlowski M.I., Skalska U., Smailus D.E.,	
RA Schieren A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT "Generation and initial analysis of more than 15,000 full-length human	
RT and mouse cDNA sequences.";	
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN [2]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Eye;	
RG NTH MGC Project;	
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.	
CC -2 R-S-SH + ROOH = R-S-S-R' + H(2)O + ROH.	
DR -1- CATALYTIC ACTIVITY: R-S-SH + ROOH = R-S-S-R' + H(2)O + ROH.	
DR EMBL; BC095755; AAHC95755_1; -; mRNA.	
DR Ensembl; ENSDARG00000020317; Danio rerio.	
DR ZFIN; ZDB-GENE-050522-159; zgc:112318.	
DR InterPro; IPR000666; APBC-TSA.	
DR InterPro; IPR012336; Thioredoxin-like.	
DR InterPro; IPR012335; Thioredoxin_fold.	
PFam; PF00578; ApBC-TSA; 1.	
KW Antioxidant; Hypothetical protein; oxidoreductase; Peroxidase;	
KW Redox-active center.	
SQ SEQUENCE: 162 AA; 17109 MN; S57C1CE753B0041 CRC64;	
Query Match 63.1%; Score 524; DB 2; Length 168;	
Best Local Similarity 65.4%; Pred. No. 1.4e-38;	
Matches 102; Conservative 18; Mismatches 34; Indels 2; Gaps 1;	
DR	
Qy 3 PIKVGDIAITAVEVEGEGPCKNVLNABLEFLGKKGVLFGVIGAFPGCCKTHLPGVQEAE 62	
Db 33 PIKVGDIAITAVEVEGEGPCKNVLNABLEFLGKKGVLFGVIGAFPGCCKTHLPGVQEAE 92	
Qy 63 LAKGVQVVAQLSINDAFTGEGWRAHKAEGKVLLADPTGAFSKETDILIDDSVLSIRG 122	
Db 93 LAKGVQVVAQLSINDAFTGEGWRAHKAEGKVLLADPTGAFSKETDILIDDSVLSIRG 150	
Qy 123 NRRLRKFSNVQDGIVKALNVEPDGGLTCSLAPNISQL 158	
Db 151 NIRSKRYSMLVEDGEVKQLVNEPDGGLTCSLAPNISQL 186	
RESULT 14	
Q50G08_ABDAB	
ID Q50G08_ABDAB PRELIMINARY; PRT; 157 AA.	
AC	
DT 01-FEB-2005 (TREMBlrel. 29, Created)	
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)	
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)	
DE Peroxiredoxin-like protein.	
OS Aedes aegypti (Yellowfever mosquito).	
OC Aedes aegypti; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Culicidae; Culicinae; Culicini; Aedes; Stegomyia.	
OX NCBI_TaxID=7159;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Salivary gland;	
RA Chandra P.K., Wikle S.K.;	
RT "Complementing the sialome of the adult female Aedes aegypti mosquito.";	
RT	

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Conjugation or reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles (By similarity).

CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R -S-S-R' + H₂O + ROH.

CC -!- SUBUNIT: Homodimer (By similarity).

DR EMBL; AY738253; AAV48533.1; -; mRNA.

DR GO; GO:0016591; F:oxidoreductase activity; IEA.

DR GO; GO:0016011; F:peroxidase activity; IEA.

DR InterPro; IPR000666; AhpC-TSA.

DR InterPro; IPR012336; Thioredoxin-like.

DR InterPro; IPR012335; Thioredoxin_fold.

DR Pfam; PF00578; AhpC-TSA; 1.

KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.

SQ SEQUENCE 157 AA; 16644 MW; 02B974DB7723DBE6 CRC64;

Query Match 59.6%; Score 494.5; DB 2; Length 157; Best Local Similarity 58.2%; Pred. No. 5e-36; Dels 3; Gaps 1; Matches 92; Conservative 26; Mismatches 37; Indels 3; Gaps 1;

QV 1 MAPTKVGDAPPAVERPVEGEGPKVNLAEFLPKGKKGVLFGVPGAFPTPGCSKTHLPGFVVEQA 60

Db 1 MVQIKEGDKPSIDLFEDSPANKVNMADLCAKKVFLAVPGAFPTPGCSKTHLPGFVYDRA 60

QY 61 EAIIKAKGKVQVACISVNDPFTVGEGRKGRKAEKGKVLADPTGAFGRKGKENDLUDDSLVI 120

Db 61 DAIKESGVQVIVCVSVNDPFVMSAWGKQHNTGKVRMLADPAATFTKOLELGAD--IPP 117

QY 121 FGNERLKRKFSMVVQDGIVKALNVERPDGIGLTCISLAPNI 158

Db 118 LGGIRSKRSMWVLEDGVISLNVEPDGTGUSCLADKI 155

RESULT 15

Q1PUM1 ANOGA

ID Q1PUM1 ANOGA PRELIMINARY; PRT; 246 AA.

AC Q1PUM1;

DT 01-MAR-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBrel. 26, Last sequence update)

DE ENSANGP000020393 (Fragment).

GN ORPNAME=ENSANGP000000017904;

OS Anopheles gambiae str. PEST.

OC Bubacryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyngota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.

OX NCBI_TaxID=180454;

RN [1]

RP NUCLEOTIDE_SEQUENCE.

RC STRAIN=PEST;

RA Anopheles Genome Sequencing Consortium;

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R -S-S-R' + H₂O + ROH.

CC EMBL; AAAB01008987; EAA01313.2; -; Genomic_DNA.

DR HSSP; P3044; 1HD2.

DR GO; GO:0016209; F:antioxidant activity; IEA.

DR InterPro; IPR008866; AhpC-TSA.

DR InterPro; IPR012336; Thioredoxin-like.

DR InterPro; IPR012335; Thioredoxin_fold.

DR Pfam; PF00578; AhpC-TSA; 1.

KW Antioxidant.

FT NON-TER 1 1

SQ SEQUENCE 246 AA; 26218 MW; 4C4CC83F50C8B2A3 CRC64;

Query Match 58.6%; Score 486.5; DB 2; Length 246; Best Local Similarity 58.9%; Pred. No. 4.2e-35; Matches 93; Conservative 22; Mismatches 40; Indels 3; Gaps 1;

QY 1 MAPTKVGDAPPAVERPVEGEGPKVNLAEFLPKGKKGVLFGVPGAFPTPGCSKTHLPGFVVEQA 60

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OM protein - protein search, using sw model
Run on: February 21, 2006, 21:57:41 ; Search time 168 Seconds
Perfect score: 830 ; Sequence: 1 MAPIKVDAIPAVEVFQGEP.....VERPDGIGLTCQLAPNTSQL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pupbaa/US07_PUBCOMB.dep: *
2: /cgn2_6/prodata/1/pupbaa/US08_PUBCOMB.dep: *
3: /cgn2_6/prodata/1/pupbaa/US09_PUBCOMB.dep: *
4: /cgn2_6/prodata/1/pupbaa/US10_PUBCOMB.dep: *
5: /cgn2_6/prodata/1/pupbaa/US11_PUBCOMB.dep: *

6: /cgn2_6/prodata/1/pupbaa/US11_PUBCOMB.dep: *
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match Length	DB ID	Description
1	830	100.0	162 4	US-10-408-765A-2152
2	830	100.0	162 5	US-10-686-157-2
3	830	100.0	205 4	US-10-276-774-173
4	830	100.0	214 4	US-10-394-136-1
5	830	100.0	214 4	US-10-408-765A-770
6	830	100.0	214 5	US-10-974-148-20
7	830	100.0	214 5	US-10-686-157-21
8	825	99.4	161 4	US-10-408-765A-2397
9	777	93.6	226 4	US-10-264-049-3514
10	767	92.4	162 5	US-10-686-157-6
11	752	90.6	162 5	US-10-686-157-4
12	747	90.0	219 5	US-10-733-923-21551
13	725	87.3	217 4	US-10-424-559-216448
14	667	80.4	150 4	US-10-263-828-97
15	573	69.0	169 5	US-10-491-183-16
16	68.6	351 5	US-10-450-763-51040	
17	524	63.1	188 5	US-10-732-923-21448
18	498	60.0	137 5	US-10-972-024-470
19	481	58.0	190 5	US-10-732-923-21547
20	479	57.7	157 6	US-11-097-143-1080
21	476.5	57.4	153 5	US-10-732-923-21451
22	475.5	57.3	175 5	US-10-732-923-21450
23	469.5	56.6	285 5	US-10-450-763-51060
24	400.5	48.3	185 5	US-10-732-923-21545
25	349	42.0	125 5	US-10-972-024-178
26	346	41.7	130 4	US-10-264-049-3474
27	332	40.0	183 4	US-10-767-701-51758

RESULT 1
US-10-408-765A-2152
; Sequence 2152, Application US/10408765A.
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,65A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2152
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-2152
Query Match 100.0%; Score 830; DB 4; Length 162;
Best Local Similarity 100.0%; Prd. No. 4; Be-85;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPIKVDAIPAVEVFQGEGPKVNLALFLPKGGKGVLFLGVPAGTPGCSKTHLPGFVEOA. 60
Db 1 MAPIKVDAIPAVEVFQGEGPKVNLALFLPKGGKGVLFLGVPAGTPGCSKTHLPGFVEOA. 60
QY 61 BALKAKGVQVACLSVNDARVFTGEGRAHKAEGKVRLLADPTGARGKGETDILLDSLVI. 120
Db 61 BALKAKGVQVACLSVNDARVFTGEGRAHKAEGKVRLLADPTGARGKGETDILLDSLVI. 120
QY 121 FGNRLKIKRSWVQDGIVKVALNVERPDGIGLTCQLAPNTSQL 162
Db 121 FGNRLKIKRSWVQDGIVKVALNVERPDGIGLTCQLAPNTSQL 162
; TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding

TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment of lung injuries and diseases, and of oxidative stress-related

TITLE OF INVENTION: disorders

FILE REFERENCE: DEC130.01CPI

CURRENT APPLICATION NUMBER: US/10/686,157

CURRENT FILING DATE: 2003-10-15

PRIOR APPLICATION NUMBER: US/6,759,194

PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: PCT/BE98/00124

PRIOR FILING DATE: 1998-08-20

PRIOR APPLICATION NUMBER: BE 1011331

PRIOR FILING DATE: 1997-08-20

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin version 3.3

SEQ ID NO 2

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-10-686-157-2

Query Match 100.0%; Score 830; DB 5; Length 162;

Best Local Similarity 100.0%; Pred. No. 4.8e-85; Mismatches 0; Indels 0; Gaps 0;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPIKYGDAIPAVEFEGEPGKVNLAELFKKKKGVLFGVGAFTPGCSKTHLPGFVEQA 60

Db 1 MAPIKVGDAIPAVEFEGEPGKVNLAELFKKKKGVLFGVGAFTPGCSKTHLPGFVEQA 60

Qy 61 EALKAKGVQVACLSVNDAFVFTGEWGRAHKAEKGKVRLADPTGAFGKETDILDDSLVSI 120

Db 61 EALKAKGVQVACLSVNDAFVFTGEWGRAHKAEKGKVRLADPTGAFGKETDILDDSLVSI 120

Qy 121 FGNRRLRKFSMVTQDGIVKALNVEPDGTGTLCSLAPNISQL 162

Db 121 FGNRRLRKFSMVTQDGIVKALNVEPDGTGTLCSLAPNISQL 162

RESULT 3

US-10-276-774-1773 Application US/10276774

; Sequence 1773, Application US/10276774

; Publication No. US20040053245A1

; GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

APPLICANT: Tang, Y., Tom et al

TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: Custom

SEQ ID NO 1773

LENGTH: 205

TYPE: PRT

ORGANISM: Homo sapiens

US-10-276-774-1773

Query Match 100.0%; Score 830; DB 4; Length 205;

Best Local Similarity 100.0%; Pred. No. 6.6e-85; Mismatches 0; Indels 0; Gaps 0;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPIKYGDAIPAVEFEGEPGKVNLAELFKKKKGVLFGVGAFTPGCSKTHLPGFVEQA 60

Db 44 MAPIKVGDAIPAVEFEGEPGKVNLAELFKKKKGVLFGVGAFTPGCSKTHLPGFVEQA 103

Qy 61 EALKAKGVQVACLSVNDAFVFTGEWGRAHKAEKGKVRLADPTGAFGKETDILDDSLVSI 120

Db 104 EALKAKGVQVACLSVNDAFVFTGEWGRAHKAEKGKVRLADPTGAFGKETDILDDSLVSI 163

121 FGNRRLRKFSMVTQDGIVKALNVEPDGTGTLCSLAPNISQL 162

RESULT 4

US-10-394-136-1

Sequence 1, Application US/10394136

Publication No. US20030175787A1

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Lal, Preeti

APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: VESICLE MEMBRANE PROTEINS

FILE REFERENCE: PC-0029 CIP

CURRENT APPLICATION NUMBER: US/10/394,136

CURRENT FILING DATE: 2003-03-19

PRIOR APPLICATION NUMBER: US/09/718,996

PRIOR FILING DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PERL Program

SEQ ID NO 1

LENGTH: 214

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. US20030175787A1 743725

US-10-394-136-1

Query Match 100.0%; Score 830; DB 4; Length 214;

Best Local Similarity 100.0%; Pred. No. 7e-85; Mismatches 0; Indels 0; Gaps 0;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPIKYGDAIPAVEFEGEPGKVNLAELFKKKKGVLFGVGAFTPGCSKTHLPGFVEQA 60

Db 53 MAPIKVGDAIPAVEFEGEPGKVNLAELFKKKKGVLFGVGAFTPGCSKTHLPGFVEQA 112

Qy 61 EALKAKGVQVACLSVNDAFVFTGEWGRAHKAEKGKVRLADPTGAFGKETDILDDSLVSI 120

Db 113 EALKAKGVQVACLSVNDAFVFTGEWGRAHKAEKGKVRLADPTGAFGKETDILDDSLVSI 172

Qy 121 FGNRRLRKFSMVTQDGIVKALNVEPDGTGTLCSLAPNISQL 162

Db 173 FGNRRLRKFSMVTQDGIVKALNVEPDGTGTLCSLAPNISQL 214

RESULT 5

US-10-408-765A-770

Sequence 770, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:

APPLICANT: Ghosh, Sounitra S.

APPLICANT: Fahy, Boin D.

APPLICANT: Zhang, Bing

APPLICANT: Gibson, Bradford W.

APPLICANT: Taylor, Steven W.

APPLICANT: Glenn, Gary M.

APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

FILE REFERENCE: 66008,465

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 770

LENGTH: 214

TYPE: PRT

ORGANISM: Homo sapiens

US-10-408-765A-770

Query Match 100.0%; Score 830; DB 4; Length 214;

Sequence 3514, Application US/10264049
 Publication No. US2004005579A1
 GENERAL INFORMATION:
 APPLICANT: BIRBE ET AL.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 CURRENT APPLICATION NUMBER: US/10/264,049
 CURRENT FILING DATE: 2002-10-04
 PRIOR APPLICATION NUMBER: PCT/US01/15569
 PRIOR FILING DATE: 2001-06-07
 PRIOR APPLICATION NUMBER: US 60/209,467
 PRIOR FILING DATE: 2000-06-07
 NUMBER OF SEQ ID NOS: 4360
 SOFTWARE: PatentIn Ver. 3.1
 SEQ ID NO 3514
 LENGTH: 225
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (79)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (90)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (110)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (143)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (190)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (203)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (225)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; US-10-264-049-3514
 Quay Match 93.6%; Score 777; DB 4; Length 226;
 Best Local Similarity 95.1%; Pred. No. 7.1e-79; Indels 0; Gaps 0;
 Matches 154; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 Other Information: Xaa equals any of the twenty naturally occurring L-amino acids
 ; US-10-264-049-3514
 RESULT 11
 US-10-686-157-6
 Query Match 92.4%; Score 767; DB 5; Length 162;
 Best Local Similarity 91.4%; Pred. No. 6.1e-78; Indels 0; Gaps 0;
 Matches 148; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 Other Information: Xaa equals any of the twenty naturally occurring L-amino acids
 ; US-10-686-157-6
 Quay 61 BALKAKGVQVACLSUNDAVTGTGKAGKURLLADPTGAFGKETIDLLDDSLVSI 120
 Db 61 GAIKAKGAQVVAACLSUNDAVTGTGKAGKURLLADPTGAFGKETIDLLDDSLVSI 120
 Db 61 GAIKAKGAQVVAACLSUNDAVTGTGKAGKURLLADPTGAFGKETIDLLDDSLVSI 120
 Db 121 FGNRRLRKFSMVKQVAKLNSVNDVPIEVGRRAHQAEKGKRLLAQPTGAFGKATDILDDSLVSI 162
 Db 121 FGNRRLRKFSMVKQVAKLNSVNDVPIEVGRRAHQAEKGKRLLAQPTGAFGKATDILDDSLVSI 162
 ; US-10-686-157-6
 Query Match 92.4%; Score 767; DB 5; Length 162;
 Best Local Similarity 91.4%; Pred. No. 6.1e-78; Indels 0; Gaps 0;
 Matches 148; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 Other Information: Xaa equals any of the twenty naturally occurring L-amino acids
 ; US-10-686-157-6
 Quay 1 MAPIKVDAIPSEVFGEPGKVNLAELFKKGKKGVLFGVGAFTPGCSKTHLPGFVEQA 60
 Db 1 MAPIKVDAIPSEVFGEPGKVNLAELFKKGKKGVLFGVGAFTPGCSKTHLPGFVEQA 60
 Quay 61 BALKAKGVQVACLSUNDAVTGTGKAGKURLLADPTGAFGKETIDLLDDSLVSI 120
 Db 61 GAIKAKGAQVVAACLSUNDAVTGTGKAGKURLLADPTGAFGKETIDLLDDSLVSI 120
 Db 61 GAIKAKGAQVVAACLSUNDAVTGTGKAGKURLLADPTGAFGKETIDLLDDSLVSI 120
 Db 121 FGNRRLRKFSMVKQVAKLNSVNDVPIEVGRRAHQAEKGKRLLAQPTGAFGKATDILDDSLVSI 162
 Db 121 FGNRRLRKFSMVKQVAKLNSVNDVPIEVGRRAHQAEKGKRLLAQPTGAFGKATDILDDSLVSI 162
 ; US-10-686-157-6
 Query Match 92.4%; Score 767; DB 5; Length 162;
 Best Local Similarity 91.4%; Pred. No. 6.1e-78; Indels 0; Gaps 0;
 Matches 148; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 Other Information: Xaa equals any of the twenty naturally occurring L-amino acids
 ; US-10-686-157-6
 Quay 52 MAPIKVDAIPSEVFGEPGKVNLAELFKKGKKGVLFGVGAFTPGCSKTHLPGFVEQA 60
 Db 52 MAPIKVDAIPSEVFGEPGKVNLAELFKKGKKGVLFGVGAFTPGCSKTHLPGFVEQA 111
 Quay 61 BALKAKGVQVACLSUNDAVTGTGKAGKURLLADPTGAFGKETIDLLDDSLVSI 120
 Db 112 BALKAKGVQVACLSUNDAVTGTGKAGKURLLADPTGAFGKETIDLLDDSLVSI 171
 Quay 121 FGNRRLRKFSMVKQVAKLNSVNDVPIEVGRRAHQAEKGKRLLAQPTGAFGKATDILDDSLVSI 162
 Db 172 FGNRRLRKFSMVKQVAKLNSVNDVPIEVGRRAHQAEKGKRLLAQPTGAFGKATDILDDSLVSI 213
 ; US-10-686-157-6
 Sequence 6, Application US/10686157
 Publication No. US20050142126A1
 GENERAL INFORMATION:
 APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
 APPLICANT: UNIVERSITE DE MONS-HAINAUT
 TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding
 TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment
 TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related
 TITLE OF INVENTION: disorders
 FILE REFERENCE: DECLE30.001CPI
 CURRENT APPLICATION NUMBER: US/10/686,157
 CURRENT FILING DATE: 2003-10-15
 PRIOR APPLICATION NUMBER: US 6,759,194
 PRIOR FILING DATE: 2000-08-15
 PRIOR APPLICATION NUMBER: PCT/BB98/00124
 PRIOR FILING DATE: 1998-08-20
 PRIOR APPLICATION NUMBER: BE 1011331
 PRIOR FILING DATE: 1997-08-20
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 4
 LENGTH: 162
 TYPE: PRT
 ORGANISM: Rattus rattus
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (17)..(17)
 OTHER INFORMATION: X = E or G
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (63)..(63)
 OTHER INFORMATION: X = L or P
 FEATURE:
 NAME/KEY: MISC FEATURE

APPLICANT: LIU, Dyung, Aina M.; YUE, Henry
 APPLICANT: ELLIOTT, Vicki S.; WARREN, Bridget A.
 APPLICANT: DUGGAN, Brendan M.; FORSYTHE, Ian J.
 APPLICANT: LEE, Ernestine A.; HARALIK, April J. A.
 APPLICANT: RAMKUMAR, Jayalaxmi; CHAWLA, Harinder K.
 APPLICANT: BAUGEN, Mariah R.; BIRCHA, Shanya D.
 APPLICANT: GORVAD, Ann E.; TRAN, Uyen K.
 APPLICANT: LI, Joana X.; YAO, Monique G.
 APPLICANT: ISON, Craig H.; GRIFFIN, Jennifer A.
 APPLICANT: LEE, SOO YEUN; CHANG, Hsin-Ru
 APPLICANT: EMERLING, Brooke M.; TANG, Y. Tom
 APPLICANT: LAL, Preeti G.; KABIL, Amy E.
 APPLICANT: MARQUIS, Joseph P.; JIANG, Xin
 APPLICANT: JACKSON, Alan A.; ZEBARJADIAN, Yeganeh
 APPLICANT: SWARNAKAR, Anita; WILSON, Amy D.
 APPLICANT: JIN, Pei; RICHARDSON, Thomas W.
 APPLICANT: BHATIA, Umesh; BURRILL, John D.
 APPLICANT: LEE, Sally; BLAKE, Julie J.
 APPLICANT: HO, Anne; ZHENG, Wenjin
 APPLICANT: GAO, Jing
 TITLE OF INVENTION: ENYMES
 FILE REFERENCE: PP-1-214 USN
 CURRENT APPLICATION NUMBER: US/10/491,183
 CURRENT FILING DATE: 2004-03-29
 PRIOR APPLICATION NUMBER: PCT/US02/31096
 PRIOR FILING DATE: 2002-09-26
 PRIOR APPLICATION NUMBER: US 60/326,388
 PRIOR FILING DATE: 2001-09-28
 PRIOR APPLICATION NUMBER: US 60/328,979
 PRIOR FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: US 60/346,034
 PRIOR FILING DATE: 2001-10-19
 PRIOR APPLICATION NUMBER: US 60/348,284
 PRIOR FILING DATE: 2001-10-26
 PRIOR APPLICATION NUMBER: US 60/338,048
 PRIOR FILING DATE: 2001-11-08
 PRIOR APPLICATION NUMBER: US 60/332,340
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: US 60/340,357
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/387,119
 PRIOR FILING DATE: 2002-06-07
 PRIOR APPLICATION NUMBER: US 60/368,799
 PRIOR FILING DATE: 2002-03-29
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 106
 SOFTWARE: PERL Program
 SEQ ID NO 16
 LENGTH: 169
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 7500495CD1
 US-10-491-183-16

Query Match 69.0%; Score 573; DB 5; Length 169;
 Best Local Similarity 100.0%; Pred. No. 4.7e-56;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	50	KTHLPGFVEQDAAKAKGKVQVWACLSNDAYFTGEMGRRAHKAGKGKVRLLADPTGAGKET	109
Db	57	KTHLPGFVEQDAAKAKGKVQVWACLSNDAYFTGEMGRRAHKAGKGKVRLLADPTGAGKET	116
Qy	110	DILDDSLVLSIFGNRRLKRFPSMVQD1CIVKALNVEPGTCUTCSLAPN1SQL	162
Db	117	DILDDSLVLSIFGNRRLKRFPSMVQD1CIVKALNVEPGTCUTCSLAPN1SQL	169

Search completed: February 21, 2006, 22:00:57
 Job time : 169 secs

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: February 21, 2006, 21:58:17 ; Search time 18 Seconds

Sequence: (without alignments) 128.157 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPIKVGDALPAVEVFVGBP.....VERPDGIGLTCQLAPNIIQL 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 108093 seqs, 14239677 residues

Total number of hits satisfying chosen parameters: 108093

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/prodata/1/pubpaal/us08 NEW PUB.pep:*

2: /cgn2_6/prodata/1/pubpaal/us06 NEW PUB.pep:*

3: /cgn2_6/prodata/1/pubpaal/us07 NEW PUB.pep:*

4: /cgn2_6/prodata/1/pubpaal/pct NEW PUB.pep:*

5: /cgn2_6/prodata/1/pubpaal/us09 NEW PUB.pep:*

6: /cgn2_6/prodata/1/pubpaal/us10 NEW PUB.pep:*

7: /cgn2_6/prodata/1/pubpaal/us11 NEW PUB.pep:*

8: /cgn2_6/prodata/1/pubpaal/us60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1 US-10-878-556A-183

Sequence 183 Application US/10878556A

Publication No. US20050266399A1

GENERAL INFORMATION:

APPLICANT: Hoffmann La-Roche Inc.

TITLE OF INVENTION: HCV regulated protein expression

FILE REFERENCE: 21762

CURRENT APPLICATION NUMBER: US10/878,556A

CURRENT FILING DATE: 2004-06-28

NUMBER OF SEQ ID NOS: 199

SOFTWARE: PatentIn version 3.1

SEQ ID NO 183

LENGTH: 214

TYPE: PRT

ORGANISM: Homo sapiens

PUBLICATION NUMBER: US 20050266399A1

DATABASE ACCESSION NUMBER: SW hum/pdx5_human

DATABASE ENTRY DATE: 1993-04-01

US-10-878-556A-183

RESULT 1 US-10-878-556A-183

Query Match 100.0%; Score 830; DB 6; Length 214;

Best Local Similarity 100.0%; Pred. No. 1.5e-78; Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 183, App

Sequence 5556, App

Sequence 22, Appl

Sequence 24, Appl

Sequence 24, Appl

Sequence 1419, Appl

Sequence 6, Appli

Sequence 4, Appli

Sequence 1038, Ap

Sequence 5, Appli

Sequence 28, Appl

Sequence 6564, Ap

Sequence 6, Appli

Sequence 516, App

Sequence 28, Appli

Sequence 4, Appli

Sequence 1121, Ap

Sequence 71, Appl

Sequence 794, App

Sequence 176, App

Sequence 111, App

Sequence 280, App

Sequence 252, App

Sequence 7, Appli

Sequence 49, Appli

Sequence 10946, A

Sequence 36, Appl

Sequence 24, Appl

Sequence 15, Appl

Sequence 10995, A

Sequence 172, Appl

Sequence 48, Appl

Sequence 394, App

Sequence 55, Appl

Sequence 56, Appl

Sequence 50, Appl

Sequence 47, Appl

Sequence 326, App

Sequence 1926, Ap

Sequence 659, App

Sequence 22, Appl

Sequence 95, Appl

Sequence 304, App

Sequence 5876, AP

Sequence 7488, AP

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/467,657
 CURRENT FILING DATE: 2003-08-11
 PRIOR APPLICATION NUMBER: GB-0103424.8
 PRIOR FILING DATE: 2001-02-12
 NUMBER OF SEQ ID NOS: 9218
 SEQ ID NO 5556
 LENGTH: 267
 TYPE: PRT
 ORGANISM: *Neisseria gonorrhoeae*
 US-10-467-657-5556

RESULT 3
 US-11-058-926-22
 ; Sequence 22, Application US/11058926
 ; Publication No. US20060030022A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BECKWITH, JONATHAN
 ; APPLICANT: ASLUND, FREDRIK
 ; APPLICANT: BESSETTE, PAUL H.
 ; APPLICANT: GEORGIOU, GEORGE
 ; APPLICANT: RITZ, DANIEL
 ; APPLICANT: LIM, JACKIE EUN-AH
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
 ; TITLE OF INVENTION: BOND CONTAINING PROTEINS IN HOST CELLS
 ; FILE REFERENCE: HMV-052-01
 ; CURRENT APPLICATION NUMBER: US/11/058, 926
 ; CURRENT FILING DATE: 2005-02-16
 ; PRIOR APPLICATION NUMBER: US/09/679, 705
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/157, 770
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/163, 939
 ; PRIOR FILING DATE: 1999-11-08
 ; PRIOR APPLICATION NUMBER: 60/166, 044
 ; PRIOR FILING DATE: 1999-11-17
 ; NUMBER OF SEQ ID NOS: 24
 ; SEQ ID NO 24
 ; LENGTH: 188
 ; TYPE: PRT
 ; ORGANISM: *Escherichia coli*
 US-11-058-926-24

Query Match 30.4%; Score 252.5; DB 6; Length 267;
 Best Local Similarity 38.5%; Pred. No. 8 6e-19;
 Matches 57; Conservative 28; Mismatches 56; Indels 7; Gaps 5;

Qy 5 KVGDAIPARVEVPE--GRPGKNUKLALFKGGKVLFGVPGAFPGCSKTHILPGFVQEAE 61
 Db 28 RYQKQVSV-VFTRVGDWTKVQSTDILFKGKVVVFLSPGATPCCSSHLPRVNLFLG 86

Qy 62 ALKAKGQVVAQCLSVNDAFVTFGEWGRAHKAEGKVRLLADPQAFGKETDLIIDDLSVSIF 121
 Db 87 AFKFGYDAIACCUSVNDTFVWAWA-KEEESNIVYMPDGNGEFTGCMGMLVGKEDLG-F 144

Qy 122 GNRRLKRFPSMWWVQDGIVKALNVEPDGTG 149
 Db 145 G-KRSWRVSMVLDGWWVKEMF1EPBEG 171

RESULT 4
 US-11-058-926-24
 ; Sequence 24, Application US/11058926
 ; Publication No. US20060030022A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BECKWITH, JONATHAN
 ; APPLICANT: ASLUND, FREDRIK
 ; APPLICANT: BESSETTE, PAUL H.
 ; APPLICANT: GEORGIOU, GEORGE
 ; APPLICANT: RITZ, DANIEL
 ; APPLICANT: LIM, JACKIE EUN-AH
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
 ; TITLE OF INVENTION: BOND CONTAINING PROTEINS IN HOST CELLS
 ; FILE REFERENCE: HMV-052-01
 ; CURRENT APPLICATION NUMBER: US/11/058, 926
 ; CURRENT FILING DATE: 2005-02-16
 ; PRIOR APPLICATION NUMBER: US/09/679, 705
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/157, 770
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/163, 939
 ; PRIOR FILING DATE: 1999-11-08
 ; PRIOR APPLICATION NUMBER: 60/166, 044
 ; PRIOR FILING DATE: 1999-11-17
 ; NUMBER OF SEQ ID NOS: 24
 ; SEQ ID NO 24
 ; LENGTH: 188
 ; TYPE: PRT
 ; ORGANISM: *Escherichia coli*
 US-11-058-926-24

Query Match 11.7%; Score 97; DB 7; Length 188;
 Best Local Similarity 28.6%; Pred. No. 0.0061; 0.0061;
 Matches 34; Conservative 20; Mismatches 53; Indels 12; Gaps 5;

Qy 38 FQVPGAFPTGCSKTHILPGFVQEAEALKAKGQVVAQCLSVNDAFVTFGEWGRAHKAEGKVR- 96
 Db 38 FVYPADFTFVC-PTELGDVADHYEELQKLGVDVVA-VSTDTHFTKAWHSSETTAKIKY 95

Qy 97 -LLADPFTGAFGKETDLIIDDLSVSIFGRRRLKRFNSWVQ-DGIVKALNVRPDGTGILCS 153
 Db 96 AMIGDPTGALTRNFNDNREDEGLA-----DRAFTVFDPOSITIONALNEVTAEGIRDAS 147

RESULT 5
 US-10-821-234-1419
 ; Sequence 1419, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andamani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821, 234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462, 047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 1419
 LENGTH: 271
 TYPE: PRT
 ORGANISM: *Homo sapiens*

Query Match 28.9%; Score 107; DB 7; Length 187;
 Best Local Similarity 28.6%; Pred. No. 0.00056;
 Matches 36; Conservative 22; Mismatches 56; Indels 12; Gaps 5;

Qy 31 KGKKGVLFGVGAFTPGCSKTHILPGFVQEAEALKAKGQVVAQCLSVNDAFVTFGEWGRAHK 90
 Db 30 EGRWSVFFPYADFTFVC-PTELGDVADHYEELQKLGVDVVA-VSTDTHFTKAWHSSE 87

Qy 91 AECKVR--LLADPFTGAFGKETDLIIDDLSVSIFGRRRLKRFNSWVQ-DGIVKALNVRPDG 147
 LENGTH: 271
 TYPE: PRT
 ORGANISM: *Homo sapiens*

US-10-821-234-1419

Query Match 11.6%; Score 96; DB 6; Length 271;
Best Local Similarity 26.8%; Pred. No. 0.013; Mismatches 30;
Matches 42; Conservative 29; MisMatches 66; Indels 20; Gaps 8;

Qy 1 MAPIKGDAIPAVE--VFEGERGKVNLAELFGKGKGLFGPGAFPGCSKTHLPGFV 57
Db 76 LSKAKKISKRPAPYMEGATVAGNDYFVPLDFTFVC-PTEIATFG 132
Qy 58 EQABALKAKGKVQVACLSNDAYFTGEGRAHKAGG---KVRLLADPTGAFGKTDLL 112
Db 133 DRLEFRSNTTEVAC-SVDSQFTHLAMINTPRQGGLGPRLPLSLTHQTSKDKGVY 191
Qy 113 LDDSLSVSIFGNRRLRKRFSMVWQDGIVK--AINTVPGD 147
Db 192 LEDS-----GHTLRLGLFIDDKGKILRQITLNDLPGV 222

RESULT 6 US-10-642-272A-6

Sequence 6, Application US/10642272A
Publication No. US20050277606A1
GENERAL INFORMATION:
APPLICANT: Hattori, FumiYuki
APPLICANT: Sugimura, Keijiro
APPLICANT: Furuya, Mayumi
TITLE OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OF INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
CURRENT APPLICATION NUMBER: US/10/642,272A
CURRENT FILING DATE: 2003-08-18
PRIORITY NUMBER: PCT/JP02/01358
PRIORITY FILING DATE: 2001-02-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 257
TYPE: PRT
ORGANISM: Mus sp.

RESULT 7 US-10-642-272A-6

Query Match 10.9%; Score 90.5; DB 6; Length 257;
Best Local Similarity 28.6%; Pred. No. 0.043; Mismatches 34; Conservative 22; MisMatches 50; Indels 13; Gaps 4;

Qy 30 FKGKKGKVIFGVPGAAFTPGCSKTHLPGFVQEAEALKAKGKVQVACLSNDAYFTGEGRAH 89
Db 91 FGKXKVLFVFFYPLDFTFVC-PTEIATFVAFPSDKANEFHDVNCENVA-VSDSHFSHLAWINTP 148
Qy 90 KAGG-----KVRLLADPTGAFGKTDLLSDVSIFGNRRLRKRFSMVWQDGIVKALGVY 143
Db 149 RKGNGGLGMNITLSDITRQISRDYGVVLESAGIALRG-----LFIIDPNGVVKHLSV 201

RESULT 8 US-10-821-234-1038

Query Match 10.8%; Score 89.5; DB 6; Length 256;
Best Local Similarity 28.6%; Pred. No. 0.055; Mismatches 34; Conservative 22; MisMatches 50; Indels 13; Gaps 4;

Qy 30 FGKKGKVIFGVPGAAFTPGCSKTHLPGFVQEAEALKAKGKVQVACLSNDAYFTGEGRAH 89
Db 90 FGKXKVLFVFFYPLDFTFVC-PTEIATFVAFPSDKANEFHDVNCENVA-VSDSHFSHLAWINTP 147
Qy 90 KAGG-----KVRLLADPTGAFGKTDLLSDVSIFGNRRLRKRFSMVWQDGIVKALGVY 143
Db 148 RKGNGGLGMNITLSDITRQISRDYGVVLESAGIALRG-----LFIIDPNGVVKHLSV 200

RESULT 9 US-10-642-272A-5

Query Match 10.8%; Score 89.5; DB 6; Length 256;
Best Local Similarity 28.6%; Pred. No. 0.055; Mismatches 34; Conservative 22; MisMatches 50; Indels 13; Gaps 4;

Qy 5 KGDAIP---AVEVFEGSRPGNKNLNLSPKGKGKVGLGVPGAFPGCSKTHLPGFVQEAE 61
Db 15 RICKPAPDFKATAVVDG-AFKEVKLSD-YKGKVVLFFYPLDFTFVC-PTEIATFSNRAE 71
Qy 62 ALXAKGKVQVACLSNDAYFTGEGRAHKAGG---KVRLLADPTGAFGKTDLLSDVSIFGNRRLRKRFSMVWQDGIVKALGVY 116
Db 72 DFRKLGEVTLG-VSVDQFTHLAWINTPREGCGLGLPLNIPILLADVTRRLSEDYGVLKTE 130
Qy 117 LNSIFG 122
Db 131 GIAVARG 136

CURRENT APPLICATION NUMBER: US/10/642,272A
 CURRENT FILING DATE: 2003-08-18
 PRIOR APPLICATION NUMBER: PCT/JP02/01358
 PRIOR FILING DATE: 2001-02-18
 PRIOR APPLICATION NUMBER: JP 41003/2001
 NUMBER OF SEQ ID NOS: 30
 SEQ ID NO 5
 LENGTH: 257
 TYPE: PRT
 ORGANISM: *Rattus norvegicus*
 US-10-642-272A-5

Query Match 10.4%; Score 86.5; DB 6; Length 257;
 Best Local Similarity 27.7%; Pred. No. 0.11; Mismatches 51; Indels 13; Gaps 4;
 Matches 33; Conservative 22; MisMatches 51; Indels 13; Gaps 4;

QY 30 RKGKKGKVLFGKGAFPGCSKTHLPGFVEQAEALKAKGQVQACLSVNDAVFTGKGRAH 89
 Db 91 RKGKYLVLPPFLPFLDFTC-PTEIIVASDKANEFHNDVYCEVVA-VSDSHSHLAWINTP 148

QY 90 KAEG----KVLILADPTGAFGKETDLDLDSLVSFGNRRLRKFSMVKQDGIVKALNV 143
 Db 149 ARNGGLGHMNTILSDTKQISRDYGVILLESAGIALRG----LPIIDPNQGVKHLV 201

RESULT 10
 US-10-642-272A-28
 ; Sequence 28, Application US/10642272A
 ; Publication No. US20050277606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hattori, Fumiyuki
 ; APPLICANT: Sugimura, Keijiro
 ; TITLE OF INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
 ; FILE REFERENCE: 58777-00012
 ; CURRENT APPLICATION NUMBER: US/10/642,272A
 ; CURRENT FILING DATE: 2003-08-18
 ; PRIOR APPLICATION NUMBER: PCT/JP02/01358
 ; PRIOR FILING DATE: 2001-02-18
 ; PRIOR APPLICATION NUMBER: JP 41003/2001
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 2
 ; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: *Rattus norvegicus*
 US-10-642-272A-28

Query Match 10.4%; Score 86; DB 6; Length 198;
 Best Local Similarity 25.4%; Pred. No. 0.089; Mismatches 53; Indels 14; Gaps 5;
 Matches 32; Conservative 27; MisMatches 53; Indels 14; Gaps 5;

QY 23 KUNLAEFLKGKKGVLFGKGAFPGCSKTHLPGFVEQAEALKAKGQVQACLSVNDAVFT 82
 Db 27 EIKLSD-YRGKVLFLPPFLDFTC-PTEIIVASDKANEFHNDVYCEVVA-VSDSHSHL 83

QY 83 GEMGRGKHAEG----KVLILADPTGAFGKETDLDLDSLVSFGNRRLRKFSMVKQDGIV 137
 Db 84 LAWINTPRKEGGGLGPUNIPLADVTKSLSONYGVKNDGIAVYRG----LPIIDAKGV 137

QY 138 VCGALV 143
 Db 138 LRQITV 143

RESULT 11
 US-10-647-657-6564
 ; Sequence 99, Application US/10467657
 ; Publication No. US2005260581A1

US-10-467-657-6564

Query Match 9.8%; Score 81; DB 6; Length 386;
 Best Local Similarity 26.6%; Pred. No. 0.72; Mismatches 41; Indels 24; Gaps 3;
 Matches 29; Conservative 15; MisMatches 41; Indels 24; Gaps 3;

QY 55 GFVEQAEALKAKGQVQACLSVNDAVFTGKGRAHKAEGKVLILADPTGAFGKED---- 110
 Db 115 GFINNIVTKFGIGVSRVSPDIN----EWKAATVANTKLFLETPSPNPLGEVADLEAL 168

QY 111 -----LLDDSLSVSFGNRRLRKFSMVKQDGIVKALNVERPDGTG 149
 Db 169 AELAHGIGALLWVDNSLLSPVGSPQIKHGADISVSKAI----DGHG 213

RESULT 12
 US-10-527-771-6
 ; Sequence 6, Application US/10527771
 ; GENERAL INFORMATION:
 ; Publication No. US20050271683A1
 ; APPLICANT: University Gent
 ; TITLE OF INVENTION: *Ostertagia* vaccine
 ; FILE REFERENCE: 2002-015
 ; CURRENT APPLICATION NUMBER: US/10/527,771
 ; CURRENT FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: US 10/243,319
 ; PRIOR FILING DATE: 2002-09-13
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: *Ostertagia ostertagi*
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (72)..(72)
 ; OTHER INFORMATION: The xaa at location 72 stands for Asn, or Thr.
 US-10-527-771-6

Query Match 9.5%; Score 79; DB 6; Length 193;
 Best Local Similarity 26.4%; Pred. No. 0.46; Mismatches 57; Indels 14; Gaps 5;
 Matches 33; Conservative 21; MisMatches 57; Indels 14; Gaps 5;

QY 24 VNLAEFLKGKKGVLFGKGAFPGCSKTHLPGFVEQAEALKAKGQVQACLSVNDAVFTG 83
 Db 23 VKLSD-YKGKYLVLPPFLDFTC-PTEIIVASDKANEFHNDVYCEVVA-VSDSHSHL 79

QY 84 EWGRGKHAEG----KVLILADPTGAFGKETDLDLDSLVSFGNRRLRKFSMVKQDGIV 138
 Db 80 AWINTPRKGKGLGDMNIPVLAQTHQIAKQDYGIVLKEDEGIAVYRG----LPIIDPKGIL 133
 QY 139 KALNV 143
 Db 134 RQITV 138

RESULT 13
 US-10-485-788A-516
 ; Sequence 516, Application US/10485788A
 ; Publication No. US20050282743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Peter S.
 ; APPLICANT: Rabinowitz, Joshua D.
 ; APPLICANT: Schweizer, Johannes
 ; APPLICANT: Carrick, Deanna Marie
 ; APPLICANT: Arbor Vita Corporation
 ; TITLE OF INVENTION: Molecular Interactions in Cells
 ; FILE REFERENCE: 20054-003240US
 ; CURRENT APPLICATION NUMBER: US/10/485, 788A
 ; CURRENT FILING DATE: 2004-02-03
 ; PRIORITY APPLICATION NUMBER: US 6/07309, 841
 ; PRIORITY FILING DATE: 2001-08-03
 ; PRIORITY APPLICATION NUMBER: US 60/360, 061
 ; PRIORITY FILING DATE: 2002-02-25
 ; PRIORITY APPLICATION NUMBER: WO PCT/US02/24655
 ; NUMBER OF SEQ ID NOS: 841
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 516
 ; LENGTH: 442
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: post-synaptic density protein 95 (PSD95)
 ; OTHER INFORMATION: Construct (N-P3) aa 1 - aa 442
 ; US-10-485-788A-516

Query Match 9.5%; Score 78.5; DB 6; Length 442;
 Best Local Similarity 27.3%; Pred. No. 1.6; Mismatches 39; Conservative 19; Mismatches 40; Indels 45; Gaps 9; Matches 39; Other Information: Description of Artificial Sequence: Synthetic

Qy 20 PGKYNLAELFGKKGVLFPGAFPGCSKTHLPGFVQEAEALKAKGVQVVAACLSVND 79
 Db 197 PAKVMEIKLKLKGPKLGFSTAG---GVSNQHPIG-----DNSI 232

Qy 80 FVTG--EWGRKAEGKV---RLADPTGAFGKETDILDDSLVSIFGNRRLKRFPSMV 133
 Db 233 YVTKTIEGGAHK--DGRLOQDKILLA--VNSVGLIE-DVMEHDAVA-----LKNTYDV 282

Qy 134 QDGIVKALNVEPDGTGTLCSLAP 156
 Db 283 YLKVAK----PSNAVLDSDYAP 300

RESULT 14
 US-11-126-313-28
 ; Sequence 28, Application US/11126313
 ; Publication No. US20050288489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirsch, Joel
 ; TITLE OF INVENTION: VOLTAGE-DEPENDENT CALCIUM CHANNEL BETA SUBUNIT FUNCTIONAL CORE
 ; FILE REFERENCE: P-6750-US
 ; CURRENT APPLICATION NUMBER: US/11/126, 313
 ; CURRENT FILING DATE: 2005-05-11
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 28
 ; LENGTH: 724
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; US-11-126-313-28

Query Match 9.5%; Score 78.5; DB 7; Length 724;
 Best Local Similarity 27.3%; Pred. No. 3; Mismatches 39; Conservative 19; Mismatches 40; Indels 45; Gaps 9; Matches 39; Other Information: Description of Artificial Sequence: Synthetic

Qy 20 PGKVNLAELFGKKGVLFPGAFPGCSKTHLPGFVQEAEALKAKGVQVVAACLSVND 79
 Db 134 QDGIVKALNVEPDGTGTLCSLAP 156
 Db 240 YLKVAK----PSNAVLDSDYAP 257

Search completed: February 21, 2006, 22:01:20
 Job time : 19 secs

Db 154 PAKVMEIKLKLKGPKLGFSTAG---GVSNQHPIG-----DNSI 189
 Qy 80 FVTG--EWGRKAEGKV---RLADPTGAFGKETDILDDSLVSIFGNRRLKRFPSMV 133
 Db 190 YVTKTIEGGAHK--DGRLOQDKILLA--VNSVGLIE-DVMEHDAVA-----LKNTYDV 239

Qy 134 QDGIVKALNVEPDGTGTLCSLAP 156
 Db 240 YLKVAK----PSNAVLDSDYAP 257

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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:46:26 ; Search time 47 Seconds

28 97 11.7 188 2 US-09-679-705-24 Sequence 24, Appli
 29 96 11.6 188 2 US-09-679-705-24 Sequence 53, Appli
 30 96 11.6 271 1 US-08-467-265-2 Sequence 2, Appli
 31 96 11.6 271 2 US-08-467-265-2 Sequence 2, Appli
 32 96 11.6 271 2 US-09-077-891-2 Sequence 2, Appli
 33 96 11.6 271 2 US-09-375-907-1 Sequence 1, Appli
 34 96 11.6 271 2 US-09-538-092-1298 Sequence 1288, Ap
 35 95 11.4 218 1 US-09-248-794A-15000 Sequence 1500, A
 36 94.5 11.4 167 2 US-09-902-541-13018 Sequence 13018, A
 37 94.5 11.4 199 2 US-09-375-907-2 Sequence 2, Appli
 38 94.5 11.4 199 2 US-09-375-907-4 Sequence 4, Appli
 39 94 11.3 196 2 US-09-134-001C-4601 Sequence 4601, Ap
 40 93.5 11.3 199 1 US-08-299-162A-2 Sequence 2, Appli
 41 93.5 11.3 199 1 US-08-467-265-14 Sequence 2, Appli
 42 93.5 11.3 199 2 US-08-467-265-14 Sequence 14, Appli
 43 93.5 11.3 199 2 US-09-407-891-14 Sequence 14, Appli
 44 93.5 11.3 199 2 US-09-538-92-1277 Sequence 1277, Ap
 91 91 11.0 195 2 US-10-197-220-101 Sequence 101, Appli

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	162	2	US-09-486-167A-2
2	830	100.0	214	2	US-09-486-167A-4
3	752	90.6	162	2	US-09-486-167A-4
4	364	43.9	125	2	US-09-513-999C-8124
5	355.5	42.8	125	2	US-09-248-794A-16927
6	315	38.0	118	2	US-09-513-999C-6299
7	252.5	30.4	189	2	US-09-959-004-8
8	241.5	29.1	202	2	US-09-540-2375
9	213.5	25.7	167	2	US-08-959-004-7
10	194	23.4	166	2	US-09-091-097-4
11	194	23.4	166	2	US-10-670-9
12	191	23.0	176	2	US-09-091-097-2
13	191	23.0	176	2	US-10-109-670-8
14	191	23.0	177	2	US-09-091-097-19
15	191	23.0	177	2	US-10-109-670-19
16	176.5	21.3	185	2	US-09-248-796A-20861
17	16.4	16.4	202	2	US-09-248-796A-20862
18	112	13.5	183	2	US-09-107-532A-8874
19	108	13.0	212	2	US-09-540-236-229
20	107	12.9	187	2	US-09-679-705-22
21	104	12.5	187	2	US-09-489-039A-3465
22	100.5	12.1	157	2	US-09-489-039A-9071
23	100.5	12.1	176	2	US-09-540-12942
24	100.5	12.1	274	2	US-09-902-540-1718
25	99.5	12.0	157	2	US-09-543-681A-8014
26	99.5	11.9	205	2	US-09-543-681A-887
27	97.5	11.7	214	2	US-09-543-681A-6147

ALIGNMENTS

RESULT 1
 US-09-486-167A-2
 Sequence 2, Application US/09486167A
 Patent No. 6759194

GENERAL INFORMATION:

APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN

TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE SEQUENCE ENCODING OF INVENTION: AND THEIR USES IN THE DIAGNOSTIC AND/OR THE TREATMENT OF DISEASES AND OF OXIDATIVE STRESS-RELATED DISORDERS

FILE REFERENCE: VANN143_001A

CURRENT APPLICATION NUMBER: US/09/486, 167A

CURRENT FILING DATE: 2000-08-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

SEQ ID NO: 2

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-486-167A-2

Query Match Best Local Similarity 100.0%; Score 830; DB 2; Length 162; Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAPIKVDAIPAVEVFGEGPKVNLALBPKGKGVLFGVGAFTPGCSKTHIPGFVQA	60
Db	1	MAPIKVDAIPAVEVFGEGPKVNLALBPKGKGVLFGVGAFTPGCSKTHIPGFVQA	60
Qy	61	EAALKAKGVQVAVCLSVNDAVFTVGEWGRHAKBCKVRLADPTGAFGKETDLDLDSLVI	120
Db	61	EAALKAKGVQVAVCLSVNDAVFTVGEWGRHAKBCKVRLADPTGAFGKETDLDLDSLVI	120
Qy	121	FGNRLRKFSMVTQDGIVKALNVEPDGNGLTCSSLAPNITISQL	162
Db	121	FGNRLRKFSMVTQDGIVKALNVEPDGNGLTCSSLAPNITISQL	162

RESULT 2

US-08-959-004-1

Sequence 1, Application US/08959004

Patent No. 6107543

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Cooley, Neil C.

APPLICANT: Lal, Preeti

APPLICANT: Shah, Purvi

APPLICANT: Kaser, Matthew

TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE

TITLE OF INVENTION: PROTEINS
 NUMBER OF SEQUNCE: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/959, 004
 FILING DATE: Herewatch
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0414 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEX:
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 214 amino acids
 STRANDEDNESS: Single
 IMMEDIATE SOURCE:
 LIBRARY: BRAITUT01
 CLOBE: 743725
 US-08-959-004-1
 Query Match 100.0%; Score 830; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 2; 5e-33;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAPIKVGDIAIPAVEVFGEPGNKVNLAELFKKGKVLFGVPGAFPTGCKHILPGFVEQA 60
 Db 53 MAPIKVGDIAIPAVEVFGEPGNKVNLAELFKKGKVLFGVPGAFPTGCKHILPGFVEQA 112
 Qy 61 BALKAKGQVQVACLSVNDAFVGEWGRAHKAEGKVRVLLADPTGAFGKETDILDDSVI 120
 Db 61 BALKAKGQVQVACLSVNDAFVGEWGRAHKAEGKVRVLLADPTGAFGKETDILDDSVI 120
 Qy 121 FENRRLKRFPSMVQDGIVKALNVEPDGTGLTSLAPNITSQL 162
 Db 121 FENRRLKRFPSMVQDGIVKALNVEPDGTGLTSLAPNITSQL 162
 RESULT 3
 US-09-486-167A-4
 Sequence 4, Application US/09486167A
 ; Patent No. 6739194
 ; GENERAL INFORMATION:
 ; APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
 ; APPLICANT: UNIVERSITE DE MONS-HAINAUT
 ; TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE SEQUENCE ENCODING SAI
 ; TITLE OF INVENTION: AND THEIR USES IN THE DIAGNOSTIC AND/OR THE TREATMENT OF LUNG IN
 ; TITLE OF INVENTION: DISEASES? AND OF OXIDATIVE STRESS-RELATED DISORDERS
 ; FILE REFERENCE: VANM43-001A
 ; CURRENT APPLICATION NUMBER: US/09/486,167A
 ; CURRENT FILING DATE: 2000-08-15
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentin version 3.0
 SEQ ID NO 4
 Patentin version 3.0
 RESULT 4
 US-09-513-999C-8124
 ; Sequence 8124, Application US/09513999C
 ; Patent No. 67391961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duxle, A.
 ; APPLICANT: Giordano, J.Y.
 ; FILE REFERENCE: 59. US2. REG
 ; CURRENT APPLICATION NUMBER: US/09/513, 999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIORITY FILING DATE: 1999-02-26
 ; PRIORITY APPLICATION NUMBER: US 60/1122,487
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patentin.pm
 ; SEQ ID NO 8124
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: 80
 ; OTHER INFORMATION: Xaa=Asp or Glu
 ; US-09-513-999C-8124
 Query Match 90.6%; Score 752; DB 2; Length 162;
 Best Local Similarity 88.9%; Pred. No. 5; 9e-84;
 Matches 144; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 MAPIKVGDIAIPAVEVFGEPGNKVNLAELFKKGKVLFGVPGAFPTGCKHILPGFVEQA 60
 Db 1 MAPIKVGDIAIPAVEVFGEPGNKVNLAELFKKGKVLFGVPGAFPTGCKHILPGFVEQA 60
 Qy 61 BALKAKGQVQVACLSVNDAFVGEWGRAHKAEGKVRVLLADPTGAFGKETDILDDSVI 120
 Db 61 BALKAKGQVQVACLSVNDAFVGEWGRAHKAEGKVRVLLADPTGAFGKETDILDDSVI 120
 Qy 121 FENRRLKRFPSMVQDGIVKALNVEPDGTGLTSLAPNITSQL 162
 Db 121 FENRRLKRFPSMVQDGIVKALNVEPDGTGLTSLAPNITSQL 162
 RESULT 5
 US-09-513-999C-8124
 Query Match 43.9%; Score 364; DB 2; Length 125;
 Best Local Similarity 98.6%; Pred. No. 1; 5e-36;
 Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MAPIKVGDIAIPAVEVFGEPGNKVNLAELFKKGKVLFGVPGAFPTGCKHILPGFVEQA 60
 Db 53 MAPIKVGDIAIPAVEVFGEPGNKVNLAELFKKGKVLFGVPGAFPTGCKHILPGFVEQA 112
 Qy 61 BALKAKGQVVA 72
 Db 113 BALKAKGQVVA 124

US-09-248-796A-16927
; Sequence 16927, Application US/09248796A
; Patent No. 6,747,137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16927
; LENGTH: 202
; TYPE: PRT
; ORGANISM: *Candida albicans*
; US-09-248-796A-16927

Query Match 42.8%; Score 355.5; DB 2; Length 202;
Best Local Similarity 44.1%; Pred. No. 3.3e-35; Mismatches 71; Conservative 25; Mismatches 60; Indels 5; Gaps 2; Matches 71

QY 4 IKGDAIPAVEVFEGEPGKVNLAELFKKGKGVLPGVPGAFPTPGCSKTHLPGFVQAEAL 63
Db 43 VSIGDKVPAVPFVPEFGSPGNDLNILABETASGKTLILGVPGKSPACSGASHVFGYKNIAP 102

QY 64 KAKGKQWVACSVNDAFVTEGGR--AHKREGKVLALAPPTGAGKETDILLDSLSVI 120
Db 103 NDKGYKORFFVVAVNDPFVTKAAGQOLLESVAGQOIRFFADSTGAFKELDLDLFDAR-KA 160

QY 121 FGNRUURKRFSMVQDGIKVAKLNVEDPGTGTCSLARNLISQ 161
Db 161 FGNERSKRYALIIEOCKVWESFVERDNTSVVSAQKVLER 201

RESULT 6
US-09-513-999C-6299
; Sequence 6299, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Ductier, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6299
; LENGTH: 118
; TYPE: PRT
; ORGANISM: *Homo sapiens*
; US-09-513-999C-6299

Query Match 38.0%; Score 315; DB 2; Length 118;
Best Local Similarity 80.7%; Pred. No. 1.4e-30; Mismatches 67; Conservative 0; Mismatches 6; Indels 10; Gaps 1; Matches 67

QY 8 DAIIPAVEVF----EGPG----NPKUNLAELFKKGKGVLPGVPGAFPTPGCSKTHLPG 55
Db 4 ERVSV-VFKTRVDRDTSVQGPNPYRWDKTYEFGGKVKVLRLPGAFPTCSNNHLPR 62

Query Match 39.8%; Score 252.5; DB 2; Length 189;
Best Local Similarity 39.8%; Pred. No. 1.3e-22; Mismatches 64; Conservative 27; Mismatches 53; Indels 17; Gaps 7; Matches 64

QY 16 SLVSTFGNRLLRKRFSMVWODGIVKALNVEDPGTGTCSLAP 156
Db 122 SNLG-FGMRSW-RYSMFWNDGKIRKMPFEPB-FGDNCPVDP 159

RESULT 8
US-09-540-236-2375
; Sequence 2375, Application US/09540236

Patient No. 6673910
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709-0000-001
 CURRENT APPLICATION NUMBER: US/09/540,236
 CURRENT FILING DATE: 2000-04-04
 NUMBER OF SEQ ID NOS: 3840
 SEQ ID NO: 2375
 LENGTH: 270
 TYPE: PRT
 ORGANISM: *M. catarrhalis*
 US-09-540-236-2375

Query Match 29.1%; Score 241.5; DB 2; Length 270;
 Best Local Similarity 39.0%; Pred. No. 4.7e-21; Mismatches 56; Indels 7; Gaps 5;
 Matches 57; Conservative 26; Mismatches 56; Indels 7; Gaps 5;

QY 7 GDAIPAVEVEGEGPNK---VNLAEFLRGKKGVLFGVPGATPGCSKTHLPGFVEQAEAL 63
 Db 29 GQKUPNA-VFHTROQDQWVQDVTDELFGKQVVFSLGAPFTCSCSTHLPYNELADEF 87

QY 64 KQKGVQVACSVNDAFTVIGENGRAHKAEGKTYRILLADPTGARGKERTDILLDSLSVIFGN 123
 Db 88 KKGIGDIDLICVSNDTFTVNNAWADDQESD-KITLIPDGNGEPTEGMNRLVSKEDLG-FG- 144

QY 124 RHLKRFMSVWVQDGIVKALNVEPDGTG 149
 Db 145 KRSWVSYMLVDDGMIVKLFDEEKG 170

RESULT 9
 US-08-959-004-7
 Sequence 7, Application US/08959004
 ; Patent No. 6137543
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Kaser, Matthew
 ; TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE
 ; TITLE OF INVENTION: PROTEINS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/959,004
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billing, Lucy J.
 ; REGISTRATION NUMBER: 35,749
 ; REFERENCE/DOCKET NUMBER: PF-0414 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-1166
 ; TELEX:
 ; ORGANISM: *M. catarrhalis*
 ; US-09-540-236-2375

Query Match 25.7%; Score 213.5; DB 2; Length 167;
 Best Local Similarity 35.3%; Pred. No. 6.3e-18; Mismatches 68; Indels 11; Gaps 6;
 Matches 60; Conservative 31; Mismatches 68; Indels 11; Gaps 6;

QY 1 MAPIKGDAIPAV-EVF---EGPGNKUNLAELFKGGKVLGCGATPGCSKTHLPGFVEQAEAL 54
 Db 1 MAPIKGDAIPAV-EVF---EGPGNKUNLAELFKGGKVLGCGATPGCSKTHLPGFVEQAEAL 54

QY 55 GFVEQAEALKAKRGVQVACSVNDAFTVIGENGRAHKAEG-KVRLIADPTGAGKETDIL 112
 Db 60 GYKRNPRILSKGVUPFLVLSQNDPFLKGKWKELGAADAKKUVFSDPNLKLKIGST 119

QY 113 LDDSLVSIGSRRRLKFRSSMTVQDGTIVKALNVEPDGTGTLTCSLARNIISQ 162
 Db 120 IDLSAIGL-GTRSGRLALIVNRSGIVEYAAIE-NGEVDVSTAQKIAKL 167

RESULT 10
 US-09-091-097-4
 Sequence 4, Application US/09091097
 ; Patent No. 6432407
 ; GENERAL INFORMATION:
 ; APPLICANT: TAKESAKO, KAZUTOH
 ; APPLICANT: OKADO, TAKASHI
 ; APPLICANT: YASIHARA, TOMOKO
 ; APPLICANT: KURODA, MASANOBU
 ; APPLICANT: ONISHI, YOSHIMI
 ; APPLICANT: KATO, IKONOSHIN
 ; APPLICANT: AKIYAMA, KAZUO
 ; APPLICANT: YASUEDA, HIROSHI
 ; APPLICANT: YAMAGUCHI, HIDEYO
 ; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
 ; TITLE OF INVENTION: MALASEZIA
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
 ; STREET: PO BOX 747
 ; CITY: FALLS CHURCH
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/091,097
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WEINER, MARC S.
 ; REGISTRATION NUMBER: 32,181
 ; REFERENCE/DOCKET NUMBER: 1422-0346P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-205-8000
 ; TELEFAX: 703-205-8050
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 166 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

GenCore version 5.1.7
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On protein - protein search, using sw model
Run on: February 21, 2006, 21:38:52 ; Search time 186 Seconds
(without alignments)

382.685 Million cell updates/sec
US-10-686-157-2
Perfect score: 830
Sequence: 1 MAPIKVQDAIPAVEVFBGEP. VREPDGTCILTCSLAPNITSQL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21;*
1: geneseqp1980s;*
2: geneseqp1990s;*
3: geneseqp2000s;*
4: geneseqp2001s;*
5: geneseqp2002s;*
6: geneseqp2003as;*
7: geneseqp2003bs;*
8: geneseqp2004as;*
9: geneseqp2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	830	100.0	162 2 AAY01079	Aay01079 Human bronchoalveolar protein; peroxisome-associated polypeptide; lung injury; oxidative stress-related disorder; inflammatory disease; cardiovascular disease; neurodegenerative disorder; allergic reaction; amyotrophic lateral sclerosis; apoptosis; high bone mass syndrome; osteoporosis; osteoporosis-pseudoglioma syndrome; diagnosis; Barret-Biedl syndrome 1; therapy.
2	830	100.0	162 7 ADJ07046	Adj07046 Human hea
3	830	100.0	205 4 ABBL1403	Abbl1403 Human Alu
4	830	100.0	214 2 AAY17388	Aay17388 Human vies
5	830	100.0	214 7 ADJ68964	Adj68964 Human hea
6	830	100.0	214 7 ADM83091	Adm83091 Human vies
7	830	100.0	214 9 ADM08846	Adw08846 Human pro
8	830	100.0	214 9 AYD81123	Ady81123 Human bra
9	830	100.0	214 9 AEA17051	AEA17051 Alzheimer
10	825	99.4	161 7 ADJ70591	Adj70591 Human hea
11	818	98.6	214 4 AAG78658	Aag78658 Human per
12	777	93.6	226 5 ABP42392	Abp42392 Human ova
13	701	84.5	194 6 ABU00319	Abu00319 Human nov
14	667	80.4	150 4 ABB87638	Abb87638 Bovine ma
15	573	69.0	169 7 ADC14210	Adc14210 Human enz
16	569	68.6	351 4 ABG20681	Abg20681 Novel hum
17	568	68.4	170 4 ABU00321	Abu00321 Human nov
18	498	60.0	137 4 ADG27703	Adg27703 Human nov
19	479	57.7	157 4 ABB63096	Abb63096 Drosophil
20	469.5	56.6	285 4 ABG04901	Abg04901 Novel hum
21	364	43.9	3 3 AGG04043	Aagg04043 Human sec
22	346	41.7	130 5 ABP42342	Abp42342 Human ova
23	315	38.0	118 3 AGG02218	Aagg02218 Human sec
24	310	37.3	8 ADM48269	Adm48269 Polypepti

25 310 37.3 248 8 ADX88783 Plant ful
26 294 35.4 162 3 AAG05212 Arabidops
27 294 35.4 179 3 AAG05211 Arabidops
28 289.5 34.9 234 8 ADT56507 Plant pol
29 289 34.8 162 3 AAG10272 Arabidops
30 288 34.7 162 3 AAG38202 Arabidops
31 288 34.7 162 7 ADL18519 Rice thio
32 288 34.7 162 7 ADL11372 Rice prot
33 288 34.7 162 7 ADL1814 Rice prot
34 288 34.7 162 7 ABM90086 Rice abio
35 288 34.7 179 3 AAG38201 Arabidops
36 286 34.5 162 3 AAG18958 Arabidops
37 286 34.5 162 3 AAG11980 Arabidops
38 286 34.5 162 3 AAG11877 Arabidops
39 286 34.5 182 3 AAG11979 Arabidops
40 280 33.7 162 7 ADL18521 Arabidops
41 277 33.4 162 3 AAG10252 Arabidops
42 277 33.4 180 3 AAG10251 Arabidops
43 263 31.7 164 7 ABM89372 Rice abio
44 259.5 31.3 126 3 AAG38450 Arabidops
45 255 30.7 160 7 ABM90200 Rice abio

ALIGNMENTS

RESULT 1
RAY01079
ID AAY01079 standard; protein; 162 AA.
AC XX
AA YAY01079;
DT 08-JUN-1999 (first entry)
DE Human bronchoalveolar polypeptide, Bl8hum.
XX
KW Bl8hum, bronchoalveolar protein, peroxisome-associated polypeptide;
KW lung injury; oxidative stress-related disorder; inflammatory disease;
KW cardiovascular disease; neurodegenerative disorder; allergic reaction;
KW amyotrophic lateral sclerosis; apoptosis; high bone mass syndrome;
KW osteoporosis; osteoporosis-pseudoglioma syndrome; diagnosis;
KW Barret-Biedl syndrome 1; therapy.
XX
OS Homo sapiens.
XX
PN W09909054-A2;
XX
PD 25-FEB-1999.
XX
20-AUG-1998; 98W0-BE000124.
XX
PR 20-AUG-1997; 97BB-00000692.
XX
PA (UYHO-) UNIV CATHOLIQUE LOUVAIN.
PA (UYHO-) UNIV MONS-HAINAUT.
XX
PI Knoops B, Hermans C, Bernard A, Wattiez R, Falmagne P;
XX
WPI: 1999-180968/15.
DR N-PRDB; AAX27965.
XX
New low molecular weight human broncho-alveolar polypeptide - useful for
PT diagnosis and/or treatment of lung injuries and diseases, and oxidative
PT stress-related diseases and disorders, especially inflammatory diseases.
XX
Claim 4; Page 33-34; 45pp; English.

This sequence is the human broncho-alveolar Polypeptide, designated Bl8hum of the invention. Bl8hum is a low molecular weight human, peroxisome-associated broncho-alveolar polypeptide. A diagnostic device featuring the polypeptide, polynucleotide and/or inhibitor is useful for in vitro detection of lung injuries and diseases or oxidative stress-related diseases and disorders, especially inflammatory diseases. The device is

CC also useful for monitoring such diseases or disorders in patients or fluid samples. The polypeptide, polynucleotide and inhibitor form pharmaceutical compositions useful in the prevention and/or treatment of these diseases or disorders, especially specific cardio-vascular diseases (e.g. atherosclerosis), neurodegenerative disorders (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral sclerosis, apoptosis and inflammatory reactions, allergic reactions (e.g. asthma, hay fever and eczema), high bone mass syndrome, osteopetrosis, osteoporosis-pseudotumor syndrome and Bader-Biedl syndrome 1. The polypeptide is also useful as a specific marker of the above diseases or disorders in a wide variety of tissues. The discovery of the peroxisome-associated polypeptide enables the development of diagnosis and treatment of peroxisomal disorders

CC Sequence 162 AA;

Query Match 100.0%; Score 830; DB 2; Length 162;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPIKGDAIIPAVEVEGEPEPKVNLAPLFFKCKKGVLFGVGAFTPGCKSKTHLPGVEQA 60
Db 1 MAPIKGDAIIPAVEVEGEPEPKVNLAPLFFKCKKGVLFGVGAFTPGCKSKTHLPGVEQA 60

Qy 61 EALKAKGQVQVACLSYNDAFVTCGEWGRHAKAGKVRLADPTGAFKGKETDILDDSVI 120
Db 61 EALKAKGQVQVACLSYNDAFVTCGEWGRHAKAGKVRLADPTGAFKGKETDILDDSVI 120

Qy 121 FGRRRLKRFPSMVQDGIVKALNVEPDGTGTCSLAPNIIQL 162

Db 121 FGRRRLKRFPSMVQDGIVKALNVEPDGTGTCSLAPNIIQL 162

RESULT 2
ADJ70346 standard; protein: 162 AA.

AC ADJ70346;
XX DT 06-MAY-2004 (first entry)

XX DE Human heat mitochondrial protein as a therapeutic target. SeqID2152.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy; diabetic acidosis and stroke; MEAS;
KW myoclonic epilepsy; ragged red fibre syndrome; MERFF; cancer;
KW neuroprotective; norotropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
OS Homo sapiens.

PN WO2003087768-A2.
XX PD 23-OCT-2003.
XX PP 04-APR-2003; 2003WO-US010870.

DT 11-JAN-2002 (first entry)
DE Human Alu co-repressor 1 homologue. SEQ ID NO:1773.

XX KW Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis; regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antirheumatic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiotonic; virucide; antibacterial; antifungal; vulnerary; antiulcer.
XX PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.

XX PT Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX DR WPI; 2003-845369/78.

PT Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, for

CC comprises detecting a modified polypeptide in a sample and correlating PT with the disease.

CC PT with the disease.

CC XX of

CC PS Claim 1; SEQ ID NO 2152; 180PP; English.

CC This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial Proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy, ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, ophthalmological, ophtalmological and cytotatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

CC Sequence 162 AA;

Query Match 100.0%; Score 830; DB 7; Length 162;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPIKGDAIIPAVEVEGEPEPKVNLAPLFFKCKKGVLFGVGAFTPGCKSKTHLPGVEQA 60
Db 1 MAPIKGDAIIPAVEVEGEPEPKVNLAPLFFKCKKGVLFGVGAFTPGCKSKTHLPGVEQA 60

Qy 61 EALKAKGQVQVACLSYNDAFVTCGEWGRHAKAGKVRLADPTGAFKGKETDILDDSVI 120
Db 61 EALKAKGQVQVACLSYNDAFVTCGEWGRHAKAGKVRLADPTGAFKGKETDILDDSVI 120

Qy 121 FGRRRLKRFPSMVQDGIVKALNVEPDGTGTCSLAPNIIQL 162

Db 121 FGRRRLKRFPSMVQDGIVKALNVEPDGTGTCSLAPNIIQL 162

RESULT 3
ADJ11403 standard; peptide; 205 AA.

AC ABB11403;
XX DT 11-JAN-2002 (first entry)

DE Human Alu co-repressor 1 homologue. SEQ ID NO:1773.

XX KW Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis; regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antirheumatic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiotonic; virucide; antibacterial; antifungal; vulnerary; antiulcer.
OS Homo sapiens.
XX PN WO200157188-A2.

XX PD 09-AUG-2001.

XX PR 05-FEB-2001; 2001WO-US0031800.

XX PR 03-FEB-2000; 2000US-00496914.

RESULT 5
 ID ADJ6964
 ID ADJ68964 standard; protein: 214 AA.
 AC AC
 XX XX
 DT 06-MAY-2004 (first entry)
 DE Human heart mitochondrial protein as a therapeutic target SeqID770.
 KW mitochondrial; human; screening assay; diabetes mellitus;
 Huntington's disease; osteoarthritis;
 Leber's hereditary optic neuropathy; LHN;
 mitochondrial encephalopathy; lactic acidosis and stroke; MELAS;
 myoclonic epilepsy; ragged red fibre syndrome; MERRF; cancer;
 neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
 osteopathic; ophthalmological; cytotatic.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghosh SS, Fahy BD, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX
 DR WPI; 2003-845369/78.
 XX
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 770; 180pp; English.
 CC This invention relates to novel mitochondrial targets that can be used
 for therapeutic intervention in treating a disease associated with
 altered mitochondrial function. Specifically, it refers to a method for
 identifying proteins of the human heart mitochondrial proteome that are
 useful for drug screening assays, as well as therapeutic targets. The
 present invention describes a method for identifying such proteins that
 can be used in the treatment of various diseases associated with altered
 mitochondrial function including diabetes mellitus, Huntington's disease,
 osteoarthritis, Leber's hereditary optic neuropathy (LHN) mitochondrial
 encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy
 ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 compositions have neuroprotective, nontropic, antidiabetic,
 anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 cytosolic activities. This polypeptide sequence is a human heart
 mitochondrial protein of the invention.
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 214 AA;
 Query Match 100.0%; Score 830; DB 7; Length 214;
 Best Local Similarity 100.0%; Pred. No. 7.3e-90; Mismatches 0; Gaps 0;
 Matches 162; Conservative 0; Mismatches 0; Indels 0;
 OY 1 MAPIKVGDAPAVENFEGEPGNKVNALBLFGKGKGVILFGVPGAPTPGGSKTHLPGFVEQA 60
 DB 53 MAPIKVGDAPAVENFEGEPGNKVNALBLFGKGKGVILFGVPGAPTPGGSKTHLPGFVEQA 112
 OY 61 EALKAKGVQVACLSVNDAFVTGEWGRAHKAEGKVRLLADPIGAFGKETDILDDSLVSI 120

RESULT 6
 ID ADM83091
 ID ADM83091 standard; protein: 214 AA.
 AC AC
 XX XX
 DT 03-JUN-2004 (first entry)
 DE Human vesicle membrane protein (VMP) 1.
 KW Vesicle membrane protein; VMP; cell proliferative disorder; cancer;
 thyroid follicular adenoma; thyroid lymphocytic thyroiditis;
 Crohn's disease; colon adenocarcinoma; breast papillomatosis;
 breast adenocarcinoma; ovary serosacaplastic carcinoma;
 ovary follicular cyst; cervix cervicitis;
 uterus serous papillary carcinoma; uterus endometrial adenocarcinoma;
 prostate adenofibromatous hyperplasia; prostate adenocarcinoma; human.
 XX
 OS Homo sapiens.
 XX
 PT Key Location/Qualifiers
 PT Region 28. .49
 /note= "Antigenic epitope"
 PT Region 66. .79
 /note= "Antigenic epitope"
 PT Region 174. .182
 /note= "Antigenic epitope"
 PT Region 193. .202
 /note= "Antigenic epitope"
 XX
 PN US2003175787-A1.
 XX
 PD 18-SEP-2003.
 XX
 PF 19-MAR-2003; 2003US-00394136.
 XX
 PR 28-OCT-1997; 97US-00959004.
 PR 22-NOV-2000; 2000US-00718996.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Hillman JL, Yue H, Lal P, Kaser MR;
 XX
 DR WPI; 2003-898530/82.
 DR N-PSDB; ADM83146.
 XX
 PT New human vesicle membrane protein 1 (VMP1), useful for preparing a
 PT composition for diagnosing, treating or preventing a disease or condition
 PT associated with expression of VMP1 e.g., cancer.
 XX
 PS Claim 15; SEQ ID NO 1; 67pp; English.
 XX
 CC The present invention provides mammalian cDNAs which encode mammalian
 vesicle membrane proteins (VMPs). The invention is useful for treating a
 CC conditions associated with decreased expression or overexpression of VMP1
 CC such as cell proliferative disorders particularly cancers of the breast,
 CC colon, ovary, uterus, prostate, adrenal gland and thyroid including
 CC thyroid follicular adenoma, thyroid lymphocytic thyroiditis, Crohn's
 CC disease, colon adenocarcinoma, breast papillomatosis, breast
 CC adenocarcinoma, ovary serosacaplastic carcinoma, ovary follicular cyst,
 CC cervix cervicitis, uterus serous papillary carcinoma, uterus endometrial
 CC adenocarcinoma, prostate adenofibromatous hyperplasia and prostate
 CC adenocarcinoma. The present sequence is human vesicle membrane protein
 (VMP).

SQ	Sequence 214 AA;	Db	113 EALKAKGQVQVACLSVNDAFVGTGEMGRAHKAEGKVRLADPTGKGKETDILDDSLVSI 172
Query Match	100.0%; Score 830; DB 7; Length 214;	Query	121 FGNRRLKRFESMVQDGVKALNVEPDGTGJLCSLAPNITSQL 162
Best Local Similarity	100.0%; Pred. No. 7.3e-90;	Db	173 FGNRRLKRFESMVQDGVKALNVEPDGTGJLCSLAPNITSQL 214
Matches	162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 7	
Qy	1 MAPIKGDAIPAVEFEGEPGNKVNLAELFGKGKGVLFGVGAFFPGCSKTHLPGFVEQA 60	Qy	ADY81123
Db	53 MAPIKGDAIPAVEFEGEPGNKVNLAELFGKGKGVLFGVGAFFPGCSKTHLPGFVEQA 60	Db	ADY81123 standard; protein; 214 AA.
Qy	61 EALKAKGQVQVACLSVNDAFVGTGEMGRAHKAEGKVRLADPTGKGKETDILDDSLVSI 120	XX	
Db	113 EALKAKGQVQVACLSVNDAFVGTGEMGRAHKAEGKVRLADPTGKGKETDILDDSLVSI 172	AC	ADY81123;
Qy	121 FGNRRLKRFESMVQDGVKALNVEPDGTGJLCSLAPNITSQL 162	XX	16-JUN-2005 (first entry)
Db	173 FGNRRLKRFESMVQDGVKALNVEPDGTGJLCSLAPNITSQL 214	DE	Human brain damage-related disorder marker, peroxiredoxin.
RESULT 7		KW	diagnosis; neurological disease; neuroprotective; nootropic;
ADW08846		KW	Alzheimer's disease; Pick's disease; Parkinson's disease; degeneration;
ID ADW08846		KW	cerebroprotective; antiparkinsonian; peroxiredoxin.
XX		OS	Homo sapiens.
AC ADW08846;		XX	
XX		PN	WO2005023088-A2.
DT 24-MAR-2005 (first entry)		XX	
XX		PD	
DB Human protein which is up-regulated in HCV-infected tissue - SEQ ID 183.		XX	
XX		PF	
KW gene targeting; hepatitis C virus infection; protein deactivation;		XX	20-SEP-2004; 2004WO-GB050012.
XX		PR	20-SEP-2003; 2003GB-00022063.
KW protein activation.		PR	23-JUN-2004; 2004GB-00014089.
XX		PR	27-AUG-2004; 2004GB-00019068.
OS Homo sapiens.		XX	
XX		PA	(UY3B-) UNIV GENEVE.
PN EP1493750-A2.		PA	(LUCR/) LUCAS B.
XX		XX	
PD 05-JAN-2005.		PI	Hochstrasser DF, Sanchez J, Lescuyer P, Allard L;
XX		XX	
PF 28-JUN-2004; 2004EP-00015098.		DR	
XX		WPI	2005-242643/25.
PR 30-JUN-2003; 2003GB-00015248.		XX	
XX		PR	Diagnosing a brain damage-related disorder or its possibility in a subject suspected of suffering from it comprises detecting at least one polypeptide such as A-FABP or its variant or mutant in a sample of body fluid.
PA (HOFFMANN LA ROCHE & CO AG F.		XX	
XX		PR	
PI Berndt P, Kilby PM, Rugman P;		XX	
XX		PR	
DR WPI; 2005-050476/06.		XX	
XX		PR	
PT New targets for an antiviral compound having at least one down- and up-regulated hepatitis C virus (HCV) polypeptide, useful in predicting outcomes, treating or preventing HCV infections.		XX	
PT		PR	
XX		PR	
PS Claim 1; SEQ ID NO 183; 346pp; English.		XX	
XX		PR	
CC The invention comprises the amino acid sequences of protein targets for anti-hepatitis C virus (anti-HCV) drugs. The human protein targets of the invention are either up-regulated or down-regulated in HCV-infected tissue. The proteins of the invention are useful in the preparation of a medicament for the treatment or prevention of HCV infection. The present amino acid sequence represents a human protein of the invention which is up-regulated in HCV-infected tissue.		XX	
CC Sequence 214 AA;		XX	
SQ		PR	
Query Match 100.0%; Score 830; DB 9; Length 214;		XX	
Best Local Similarity 100.0%; Pred. No. 7.3e-90;		PR	
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		XX	
Qy 1 MAPIKGDAIPAVEFEGEPGNKVNLAELFGKGKGVLFGVGAFFPGCSKTHLPGFVEQA 60		Db	53 MAPIKGDAIPAVEFEGEPGNKVNLAELFGKGKGVLFGVGAFFPGCSKTHLPGFVEQA 112
Qy 61 EALKAKGQVQVACLSVNDAFVGTGEMGRAHKAEGKVRLADPTGKGKETDILDDSLVSI 120		Qy	61 EALKAKGQVQVACLSVNDAFVGTGEMGRAHKAEGKVRLADPTGKGKETDILDDSLVSI 172
Db 61 EALKAKGQVQVACLSVNDAFVGTGEMGRAHKAEGKVRLADPTGKGKETDILDDSLVSI 120		Db	61 EALKAKGQVQVACLSVNDAFVGTGEMGRAHKAEGKVRLADPTGKGKETDILDDSLVSI 172
Qy 61 EALKAKGQVQVACLSVNDAFVGTGEMGRAHKAEGKVRLADPTGKGKETDILDDSLVSI 120		Db	

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OM protein - protein search, using SW model

Run on: February 21, 2006, 21:42:32 ; Search time 39 Seconds

Sequence: 1 MAPIKVGDALPAVEVFVFGEP.....VERPDGTLTCSLAPNITSQL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: Pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	630.5	76.0	209	JCT7239	peroxiredoxin V -
2	317	38.7	191	2 AB3434	thiol peroxidase (
3	312.5	37.7	160	2 H87669	AlpC/TSA family pr
4	303	36.5	161	2 C97454	hypothetical prote
5	303	36.5	161	2 AB2672	peroxiredoxin [imp
6	297.5	35.8	157	2 DR2209	probable antioxida
7	294	35.4	162	2 B86684	hypothetical prote
8	289.5	34.9	234	2 T47553	peroxiredoxin-like
9	286	34.5	162	2 A96684	hypothetical prote
10	275.5	33.2	251	2 A91998	peroxiredoxin 2 fa
11	252.5	30.4	189	2 S74815	membrane protein -
12	250.5	30.2	245	2 Q81140	peroxiredoxin 2 fa
13	243	29.3	247	2 DR2051	peroxiredoxin fami
14	225.5	27.2	243	2 AB0477	probable peroxired
15	219.5	26.4	241	2 164154	conserved hypothet
16	219	26.4	217	2 AB2871	hypothetical 21.4K
17	219	26.4	212	2 G97647	peroxisomal membra
18	216	26.0	156	2 T41316	peroxisomal membra
19	213.5	25.7	167	2 A32646	hypothetical prote
20	210	25.3	553	2 D96684	conserved hypothet
21	209.5	25.2	179	2 S39907	peroxisomal membra
22	208.5	25.1	167	2 B32646	hypothetical prote
23	194	23.4	164	2 G36632	allergen Mal f3 -
24	191.5	23.1	166	2 JF0227	allergen Mal f2 -
25	191	23.0	177	2 JF0226	hypothetical prote
26	147	17.7	176	2 S64946	probable antioxi
27	115	13.9	195	2 T39667	alkyl hydroperoxid
28	114.5	13.8	215	2 S74033	B15C protein - bar
114	13.7				

ALIGNMENTS

RESULT 1
JCT7239
peroxiredoxin V - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: JCT7239
R;Lee, T.H.; Kim, S.J.; Kang, S.W.; Lee, K.K.; Rhee, S.G.; Yu, D.Y.
Biocel. Biophys. Res. Commun. 270, 356-362, 2000
A;Title: Molecular cloning and characterization of the mouse peroxiredoxin V gene.
A;Reference number: JCT7239
A;Accession: JCT7239
A;Residues: 1-209 <LE>
A;Experimental source: liver
C;Comment: This protein, thiol-specific antioxidant, belonging to peroxiredoxin family, operates, and influences the differentiation, proliferation, activity and survival of C;Genetics:
A;Gene: proxv
A;Map position: 19
A;Introns: 53/3; 98/2; 141/3; 154/3; 175/2
C;Keywords: liver

Query Match 76.0%; Score 630.5; DB 2; Length 209;

Best Local Similarity 78.0%; Pred No. 6.1e-51;

Matches 131; Conservative 6; NMatches 16; Indels 13; Gaps 2;

Matches 131; Conservative 6; NMatches 16; Indels 13; Gaps 2;

Query 1 MAPIKVGDALPAVEVFGRGKGNKLAELFGKKGKVLFVGPGATPGCCSKTHL-----P 54
Db 49 MAPIKVGDALPAVEVFGRGKGNKLAELFGKKGKVLFVGPGATPGCCSKTHL-----P 54
QY 55 GFVEQABALKAGKGVVACLSVNDAVFTGEGRAKKAEGKVLADPTGAGPKETDLD 114
Db 102 GFVEQAGALKAGKGVVACLSVNDAVFTGEGRAKKAEGKVLADPTGAGPKETDLD 161
QY 115 DLSVLSIFGNRKLKRISMMWVQDGIVKALNYPEDGTLTCSLAPNITSQL 162
Db 162 DLSVLSIFGNRKLKRISMMWVQDGIVKALNYPEDGTLTCSLAPNITSQL 209

RESULT 2
AB3434
thiol peroxidase (EC 1.11.1.-) [imported] - *Brucella melitensis* (strain 16M)

C;Species: *Brucella melitensis*
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3434
R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, M.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagiwara, S.; O'Callaghan, D.; Detessi, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A;Reference number: AD352; PMID:11756688
A;Accession: AB3434

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-191 <KUR>
 A;Cross-references: UNIPROT:Q8YFR4; UNIPARC:UPI000058096; GB:AE008917; PIDN:AAL52637.1;
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BM11456
 A;Map position: I
 C;Keywords: oxidoreductase

Query Match 38.2%; Score 317; DB 2; Length 191;
 Best Local Similarity 42.9%; Pred. No. 5.3e-22; Mismatches 58; Indels 4; Gaps 2;
 Matches 69; Conservative 30; Mismatches 58; Indels 4; Gaps 2;

QY 4 IKVGDATPAV--EVPEGPNGNKUNLASELFKGKGVLGPGVAPTPGCSKTHLPGFVEQAE 61
 Db 33 IKVGDRLPATPKVKTADGVTEMTDDVFKGRKVLFVAPGAAFTPTCISLNHLPGYLNRD 92

QY 62 ALKAKGQVVAQCLSYNDAFVGEWGRAHKAEGKVRLLADPTGAFGKETDILDDSVSIF 121
 Db 93 ATLAKGVTQIAWVNDPFWGMAWAOSTGGKILFLADGFTKAGLIDLSGGI- 151

QY 122 GNRRLKEFSMWMQDGIVKALNVEPDGIGLTCISLAPNITSQI 162
 Db 152 -GVRSKRYSVAVEDGVVVKSLNTEEQPGQAVISAASALLAQI 191

RESULT 3

H87669 AhpCTSA Family protein [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: H87669

R;Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haff, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Ventner, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: H87669
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-160 <STO>
 A;Cross-references: UNIPROT:Q9A312; UNIPARC:UPI0000C7A6D; GB:AE005673; NID:gi1425104; E
 C;Genetics:
 A;Gene: CC3394

Query Match 37.7%; Score 312.5; DB 2; Length 160;
 Best Local Similarity 45.1%; Pred. No. 1.1e-21; Mismatches 73; Conservative 21; Indels 61; Gaps 4;
 Matches 73; Conservative 21; Mismatches 61; Indels 7; Gaps 4;

QY 4 IKVGDATPAVVEP--EGRPGNKUNLASELFKGKGVLGPGVAPTPGCSKTHLPGFVEQAE 61
 Db 3 IKVGDTPATPKVKTADGVTEMTDDVFKGRKVLFVAPGAAFTPTCISLNHLPGYLNRD 62

QY 62 ALKAKGQVVAQCLSYNDAFVGEWGRAHKAEGKVRLLADPTGAFGKETDILDDSVSIF 121
 Db 63 ELAKGVTQIAWVNDPFWGMAWAOSTGGKILFLADGFTKAGLIDLSGGI- 119

QY 122 G-NRRLKEFSMWMQDGIVKALNVEPDGIGLTCISLAPNITSQI 162
 Db 120 GMGARSQRYSLVAKDGVTQIAWV-DAGQFKVSSAEVLEQI 160

RESULT 4

C97454 hypothetical protein AGR_C1423 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C;Species: Agrobacterium tumefaciens
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: C97454

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, R.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Happas, C.; Markez, B.; Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: C07454
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-161 <KUR>
 C;Genetics:
 A;Map position: circular chromosome

Query Match 36.5%; Score 303; DB 2; Length 161;
 Best Local Similarity 44.7%; Pred. No. 8.5e-21; Mismatches 72; Conservative 22; Indels 4; Gaps 2;
 Matches 72; Conservative 22; Mismatches 63; Indels 4; Gaps 2;

QY 4 IKVGDATPAVVEP--EGRPGNKUNLASELFKGKGVLGPGVAPTPGCSKTHLPGFVEQAE 61
 Db 3 IKIGEKPASATPKVKTADGVTEMTDDVFKGRKVLFVAPGAAFTPTCISLNHLPGYLNRD 62

QY 62 ALKAKGQVVAQCLSYNDAFVGEWGRAHKAEGKVRLLADPTGAFGKETDILDDSVSIF 121
 Db 63 ALAKGVTQIAWVNDPFWGMAWAOSTGGKILFLADGFTKAGLIDLSGGI- 120

QY 122 GNRRLKEFSMWMQDGIVKALNVEPDGIGLTCISLAPNITSQI 162
 Db 121 LGVRSKRYSVAVEDGVVVKSLNVEENPGQATVSAAMIEQL 161

RESULT 5

AB2672 peroxiredoxin [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AB2672

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 an, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
 A;Authors: Yoo, B.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.W.; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AB2672
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-161 <KUR>
 A;Cross-references: UNIPROT:Q8UHA4; UNIPARC:UPI000001911; GB:AE008688; PIDN:AAL41795.1;
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu0779
 A;Map position: circular chromosome

Query Match 36.5%; Score 303; DB 2; Length 161;
 Best Local Similarity 44.7%; Pred. No. 8.5e-21; Mismatches 72; Conservative 22; Indels 4; Gaps 2;
 Matches 72; Conservative 22; Mismatches 63; Indels 4; Gaps 2;

QY 4 IKVGDATPAVVEP--EGRPGNKUNLASELFKGKGVLGPGVAPTPGCSKTHLPGFVEQAE 61
 Db 3 IKIGEKPASATPKVKTADGVTEMTDDVFKGRKVLFVAPGAAFTPTCISLNHLPGYLNRD 62

QY 62 ALKAKGQVVAQCLSYNDAFVGEWGRAHKAEGKVRLLADPTGAFGKETDILDDSVSIF 121
 Db 63 ALAKGVTQIAWVNDPFWGMAWAOSTGGKILFLADGFTKAGLIDLSGGI- 120

QY 122 GNRRLKEFSMWMQDGIVKALNVEPDGIGLTCISLAPNITSQI 162
 Db 121 LGVRSKRYSVAVEDGVVVKSLNVEENPGQATVSAAMIEQL 161

RESULT 6

DB2209 probable antioxidant VCI350 [imported] - Vibrio cholerae (strain N16961 serogroup 01)
 C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: DB2209
 R;Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Charddon, D.; Birmolaeva, M.D.; Vaithianathan, J.; Babb, S.; Qin, H.; Dragoi, I.; Sellers, E.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 403, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-157 <HEI>
 A;Cross-references: UNIPROT:Q9KSA9; UNIPARC:UPI0000023FFC; GB:AB004215; GB:AE003852; NID: C;Genetics:
 A;Experimental source: serogroup O1; strain: N1691; biotype El Tor
 A;Gene: VCL350
 A;Map position: 1

Query Match 35.8%; Score 297.5; DB 2; Length 157;
 Best Local Similarity 41.6%; Pred. No. 2.7e-20;
 Matches 67; Conservative 29; Mismatches 58; Indels 7; Gaps 4;
 Db 119 KDKGKGV---RSRFAFLDVKVTVANVESEGR-FTVSSADDILKAL 162

QY 4 IKVGKDIAPIAVEVFE--GEPGNKVNLAELFKGKGKGVLFGVGRGFTPGCSKTHLPGFVEQAE 61
 2 1QIGQTLPDVQIJSORTSEGTHSSTLFRANKKVVLFAVFGAFTPTCSSEAHLPGVVLAD 61

Db 62 ALKAKGQVQVVAQCLSYNDAFTVGEWGRAHKAGKGKVLLADPTGAFKETDILLLDLSIVSIF 121
 62 KPKKEKGVDMICAVSVNDAFVKAQWGAQNA-SEIAMLADGIDASFTKALGLEMDD--TGNF 117

QY 122 GARRUKRKFMSVQVQDGIVKALNVEPDTGTLGTCSSLANIIQL 162
 118 GGVRSQSYAVMVIENNVVTLNVEPPTK-FELSKAETVLSL 157

RESULT 7

B96684 hypothetical protein F12P19.14 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: B96684
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Ansens, N.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurob, J.S.; Maiti, R.; Marzali, I.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwarz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Tittle, Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: B96684
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-162 <STO>
 A;Cross-references: UNIPROT:Q9XEX2; UNIPARC:UPI00000A6C36; GB:AB005173; NID:96227022; PI: C;Genetics:
 A;Gene: F12P19.14
 A;Map position: 1

Query Match 35.4%; Score 294; DB 2; Length 162;
 Best Local Similarity 41.4%; Pred. No. 5.8e-20;
 Matches 70; Conservative 26; Mismatches 59; Indels 14; Gaps 6;

QY 1 MAPKVGDAPI--AVRVP-EGEPGNKVNLAELFKGKGKGVLFGVGRGFTPGCSKTHLPGFV 57
 1 MAPIANGDVFVPGDTISFPFDENDQLOTAWSHSLAGKVKVILFGVPGAFPTCSMKHVKVPGFI 60

Db 58 EQAEALKAKGQVQVVAQCLSYNDAFTVGEWGRAHKAGKGKVLLADPTGAF---GKETDIL 113
 61 EKAEELRKGKGVDICAVSVNDAFVKAQWGAQNA-SEIAMLADGIDASFTKALGLEMDD-L 118

RESULT 8

T47553 peroxiredoxin-like protein - *Arabidopsis thaliana*
 N;Alternative names: protein F8J2.130
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: T47553
 R;Nakamura, G.; Partmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Mayer, K.F.X.
 A;Submitted to the Protein Sequence Database, April 2000
 A;Reference number: 224458
 A;Accession: T47553
 A;Molecule type: DNA
 A;Residues: 1-234 <NYA>
 A;Cross-references: UNIPROT:Q9L9F6; UNIPARC:UPI00000AC168; EMBL:AL132969
 A;Experimental source: cultivar Columbia; BAC clone F8J2
 C;Genetics:
 A;Map position: 3
 A;Note: F8J2.130

Query Match 34.9%; Score 289.5; DB 2; Length 234;
 Best Local Similarity 40.8%; Pred. No. 2.4e-19;
 Matches 69; Conservative 29; Mismatches 58; Indels 13; Gaps 5;

Db 71 ASIVGDKUPDSTSYPDLSPTGDVTVTWSLTTAGKKTILFAVFGAFTPTCOSKRVFPGFV 130

QY 2 APIKGDAPIAVEVFEVFGFEGF---NKNVLAELFKGKGKGVLFGVPGAFPTCSKTHLPGFV 57
 114 DDSLVSIFGNRRLKRFMSVQVQDGIVKALNVEPDTGTLGTCSSLANIIQL 162

Db 189 RDKPVGL--GVRSSRYALIADDGVVKVNL-EGGAFNTSSADEMLKAL 234

QY 58 EQAEALKAKGQVQVVAQCLSYNDAFTVGEWGRAHKAGKGKVLLADPTGAF---GKETDIL 113
 131 SKAGBLRKGKGVDVACISNDAFVMEARKDGLGINDENVWLSIDNGEFTGKGVLD-L 188

Db 114 DDSLVSIFGNRRLKRFMSVQVQDGIVKALNVEPDTGTLGTCSSLANIIQL 162

QY 71 ASIVGDKUPDSTSYPDLSPTGDVTVTWSLTTAGKKTILFAVFGAFTPTCOSKRVFPGFV 130

Db 189 RDKPVGL--GVRSSRYALIADDGVVKVNL-EGGAFNTSSADEMLKAL 234

RESULT 9

A96684 hypothetical protein F12P19.13 [imported] - *Arabidopsis thaliana* (mouse-ear cress)
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A96684
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Ansens, N.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurob, J.S.; Maiti, R.; Marzali, I.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwarz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Tittle, Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A96684
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-162 <STO>
 A;Cross-references: UNIPROT:Q9SRZ4; UNIPARC:UPI00000BEB3; GB:AB005173; NID:96227021; PI: C;Genetics:
 A;Gene: F12P19.13
 A;Map position: 1

Query Match 34.5%; Score 286; DB 2; Length 162;
 Best Local Similarity 40.2%; Pred. No. 3.2e-19;
 Matches 68; Conservative 29; Mismatches 58; Indels 14; Gaps 6;

RESULT 10
AG1998 peroxiredoxin 2 family protein/glutaredoxin [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG1998
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.; Nakazaki, N.; Shimojo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG1998
A;Status: Preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q8YWR3; UNIPARC:UPI00000CB11; GB:BA000019; PIDN:BA077907.1;
A;Experimental source: strain PCC 7120
A;Genetics: all1541

RESULT 11
574815 membrane protein - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein Sll1621
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74315
R;Kaneko, T.; Sato, S.; Korami, H.; Tanaka, A.; Asamiu, R.; Nakamura, Y.; Miyajima, N.; K.; Okumura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74815
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-189 <KAN>
A;Cross-references: UNIPROT:P73728; UNIPARC:UPI000013AF3E; EMBL:D90909; GB:AB001339; NID: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
Query Match 30.4%; Score 252.5; DB 2; Length 189;